

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 24, 2005, 15:51:22 ; Search time 196 Seconds  
(without alignments)  
672.249 Million cell updates/sec

Title: US-10-063-553-48

Perfect score: 1215  
Sequence: 1 MTCCEGWTSCNGFSLVLL.....IVIGFLGCLCGVSKRSQIV 229

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : UniProt\_02:\*  
1: uniProt\_sprot:\*  
2: uniProt\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1215	100.0	229	2 Q6UWS1	Q6uws1 homo sapien
2	1215	100.0	229	2 AAQ89034	AaQ89034 homo sapi
3	1205	99.2	229	2 Q9H5X9	Q9h5x9 homo sapien
4	924.5	76.1	226	2 Q9CQY8	Q9cqy8 m mus muscu
5	918.5	75.6	226	2 Q9D3Q0	Q9d3q0 mus musculu
6	912.5	75.1	226	2 Q9D3R0	Q9d3r0 mus musculu
7	182	15.0	197	2 Q7SYW6	Q7syw6 xenopus lae
8	173	14.2	197	2 Q6FHF6	Q6fhf6 homo sapien
9	170	14.0	197	2 Q6IB79	Q6ib79 homo sapien
10	170	14.0	197	2 AAH69519	AaH69519 homo sapi
11	170	14.0	197	2 CAG33206	Cag33206 homo sapi
12	170	14.0	202	1 T4S1_HUMAN	P30408 homo sapien
13	170	14.0	202	2 CAG33234	Cag33234 homo sapi
14	170	14.0	202	2 Q8NE91	Q8ne91 homo sapien
15	169	13.9	201	2 Q6DHT3	Q6dht3 brachydanio
16	166.5	13.7	202	1 T4S4_HUMAN	P48230 homo sapien
17	166.5	13.7	202	2 AAP36098	Aap36098 homo sapi
18	166	13.7	197	1 T4S5_HUMAN	Q6dbq4 brachydanio
19	163.5	13.5	198	2 Q6DBQ4	Q6dbq4 brachydanio
20	160.5	13.2	202	2 Q9EQJ5	Q9eqj5 rattus norv
21	160	13.2	202	1 T4S1_MOUSE	Q64302 mus musculu
22	160	13.2	202	2 BAC36752	Bac36752 mus muscu
23	157.5	13.0	202	2 Q91XD3	Q91xd3 mus musculu
24	151.5	12.5	196	2 Q9D8G1	Q9d8g1 mus musculu
25	151.5	12.5	196	2 Q91XF2	Q91xf2 mus musculu
26	141.5	11.6	202	2 Q6P8F0	Q6p8f0 xenopus tro
27	141.5	11.6	202	2 AAH61278	AaH61278 xenopus t
28	140	11.5	124	2 Q9DFD3	Q9dfd3 oncorhynchu
29	136	11.2	202	1 T4S1_MESAU	P49111 mesocricetu
30	136	11.2	202	2 AAA80343	AaA80343 mesocrice
31	133	10.9	202	2 Q60548	Q60548 mesocricetu

32	126	10.4	201	2 Q96CE8	Q96ce8 homo sapien
33	111.5	9.2	209	2 Q96DZ7	Q96dz7 homo sapien
34	103	8.5	1448	2 Q8T683	Q8t683 dictyosteli
35	101	8.3	450	2 Q9D8F3	Q9d8f3 m mus muscu
36	100.5	8.3	242	2 Q8TNE9	Q8tne9 methanobarc
37	100	8.2	505	2 Q89HF9	Q89hf9 bradyrhizob
38	99	8.1	351	2 Q8CCV8	Q8ccv8 mus musculu
39	95.5	7.9	587	2 Q86JTS	Q86jts dictyosteli
40	94.5	7.8	416	2 Q6CTF7	Q6ctf7 kluyveromyc
41	94.5	7.8	750	2 Q8H4T2	Q8h4t2 oryza sativ
42	92	7.6	358	2 Q9U2L6	Q9u2l6 caenorhabdi
43	91	7.5	365	2 Q73LB7	Q73lb7 treponema d
44	91	7.5	365	2 AAS12462	AaA12462 treponema
45	91	7.5	382	2 Q8EBM5	Q8ebm5 shewanella
46	90.5	7.4	610	1 YFBS_ECOLI	P77741 escherichia
47	90.5	7.4	610	2 Q8FFJ4	Q8ffj4 escherichia
48	90.5	7.4	1036	2 Q7VLE5	Q7vle5 haemophilus
49	90.5	7.4	1044	2 Q6LGT2	Q6lgt2 photobacter
50	90.5	7.4	1044	2 CAG23498	Cag23498 photobact
51	89.5	7.4	310	2 Q9PMF4	Q9pmf4 campylobact
52	89	7.3	275	2 Q81655	Q81655 hemerocalli
53	89	7.3	318	2 Q86UG8	Q86ug8 homo sapien
54	88.5	7.3	319	2 Q76434	Q76434 caenorhabdi
55	88.5	7.3	568	2 Q9YLE7	Q9yle7 human immun
56	88	7.2	148	2 Q65095	Q65095 picea maria
57	88	7.2	309	2 Q6GJ51	Q6gj51 staphylococ
58	88	7.2	1036	2 Q9KVI2	Q9kvi2 vibrio chol
59	87.5	7.2	282	2 Q7ZTS1	Q7zts1 brachydanio
60	87	7.2	470	2 Q76BF8	Q76bf8 oryzias lat
61	87	7.2	470	2 BAD17898	Bad17898 oryzias l
62	86.5	7.1	891	2 Q9KN09	Q9kn09 vibrio chol
63	86	7.1	283	2 Q8YSB1	Q8ysb1 listeria mo
64	86	7.1	283	2 Q71XP0	Q71xp0 listeria mo
65	86	7.1	283	2 AAT04925	AaT04925 listeria
66	86	7.1	438	2 Q26076	Q26076 helicobacte
67	86	7.1	751	2 Q8MN62	Q8mn62 dictyosteli
68	86	7.0	239	2 Q9NB10	Q9nb10 manduca sex
69	85.5	7.0	271	1 LGT_VIBCH	Q87077 vibrio chol
70	85.5	7.0	453	1 TDE2_HUMAN	Q9nrx5 homo sapien
71	85	7.0	283	2 Q929F6	Q929f6 listeria in
72	85	7.0	328	2 Q6PHE1	Q6phe1 brachydanio
73	85	7.0	328	2 AAH56587	AaH56587 brachydan
74	85	7.0	379	1 CYB_PHAAP	Q8m706 phacochoeru
75	85	7.0	379	2 Q36471	Q36471 phacochoeru
76	85	7.0	557	2 Q7XR17	Q7xri7 oryza sativ
77	84.5	7.0	156	2 Q65096	Q65096 picea maria
78	84.5	7.0	280	2 Q65061	Q65061 picea maria
79	84.5	7.0	380	1 CXAI_BRARE	Q57474 brachydanio
80	84.5	7.0	381	2 AAQ17183	AaQ17183 brachydan
81	84.5	7.0	381	2 AAQ62128	AaQ62128 brachydan
82	84.5	7.0	382	2 Q73863	Q73863 danio aegui
83	84.5	7.0	610	2 Q7C0P8	Q7c0p8 shigella fl
84	84.5	7.0	610	2 Q83QS3	Q83qs3 shigella fl
85	84	6.9	286	2 Q8Z4A9	Q8z4a9 salmonella
86	84	6.9	352	1 QPSD_ZOSOP	Q9ygy9 zosteriasees
87	84	6.9	438	2 Q9ZJF8	Q9zjf8 helicobacte
88	84	6.9	3056	2 Q81639	Q81639 plasmodiun
89	83.5	6.9	142	2 Q8HIT9	Q8hi9 halterapis
90	83.5	6.9	331	2 Q8KKE7	Q8kke7 vibrio chol
91	83.5	6.9	560	2 Q83DX2	Q83dx2 coxiella bu
92	83.5	6.9	752	2 Q6LRB1	Q6lrb1 photobacter
93	83.5	6.9	752	2 CAG20165	Cag20165 photobact
94	83	6.8	271	1 LGT_VIBVU	Q8der8 vibrio vuln
95	83	6.8	271	1 LGT_VIBVY	Q7mnv7 vibrio vuln
96	83	6.8	332	2 Q76431	Q76431 caenorhabdi
97	83	6.8	342	2 Q9PT67	Q9pt67 xenopus lae
98	83	6.8	451	2 Q6BPX5	Q6bpx5 debaryomyce
99	82.5	6.8	138	2 Q6X9S5	Q6x9s5 allodapula
100	82.5	6.8	138	2 AAP81930	AaP81930 allodapul
101	82.5	6.8	154	2 Q9SPX7	Q9spx7 picea abies
102	82.5	6.8	180	1 PTG_HUMAN	Q9spk7 homo sapien
103	82.5	6.8	289	2 Q9DSD5	Q9deds human herpe
104	82.5	6.8	1627	2 Q8GU51	Q8gu51 oryza sativ

105	82.5	6.8	1628	2	Q7XTT6	Q7xtt6 oryza sativ	178	80	6.6	379	2	Q9MEF7	Q9mef7 martes amer
106	82	6.7	286	2	Q9XC80	Q9xc80 salmoneila	179	80	6.6	379	2	AAQ05992	AAq05992 sus scrof
107	82	6.7	286	2	Q7CPX6	Q7cpX6 salmoneila	180	80	6.6	379	2	AAQ06005	AAq06005 sus scrof
108	82	6.7	318	2	Q86UG9	Q86ug9 homo sapien	181	80	6.6	379	2	AAQ06018	AAq06018 sus scrof
109	82	6.7	379	2	Q85C79	Q85c79 sus scrofa	182	80	6.6	379	2	AAQ06044	AAq06044 sus scrof
110	82	6.7	572	2	Q7XUES	Q7xues oryza sativ	183	80	6.6	379	2	AAQ06057	AAq06057 sus scrof
111	82	6.7	804	2	Q80XB3	Q80xb3 mus musculu	184	80	6.6	379	2	AAQ06070	AAq06070 sus scrof
112	82	6.7	808	2	Q70W02	Q70w02 ciona intes	185	80	6.6	379	2	AAQ06083	AAq06083 sus scrof
113	82	6.7	808	2	CAD58841	Cad58841 ciona int	186	80	6.6	379	2	AAQ06096	AAq06096 sus scrof
114	82	6.7	809	2	Q80XB2	Q80xb2 mus musculu	187	80	6.6	379	2	AAQ06109	AAq06109 sus scrof
115	82	6.7	823	2	Q80XB6	Q80xb6 mus musculu	188	80	6.6	379	2	AAQ06122	AAq06122 sus scrof
116	82	6.7	827	2	Q8CDK8	Q8cdk8 mus musculu	189	80	6.6	379	2	AAQ06148	AAq06148 sus scrof
117	82	6.7	834	2	Q8BH12	Q8bh12 mus musculu	190	80	6.6	379	2	AAQ06161	AAq06161 sus scrof
118	82	6.7	842	2	Q8R056	Q8r056 mus musculu	191	80	6.6	379	2	AAQ06187	AAq06187 sus scrof
119	82	6.7	867	1	PML1 MOUSE	Q54990 mus musculu	192	80	6.6	379	2	AAQ06200	AAq06200 sus scrof
120	82	6.7	976	2	Q6FKX5	Q6fkx5 candida gla	193	80	6.6	379	2	AAQ06213	AAq06213 sus scrof
121	81.5	6.7	156	2	Q65097	Q65097 picea maria	194	80	6.6	379	2	AAQ06226	AAq06226 sus scrof
122	81.5	6.7	289	2	P88902	P88902 human herpe	195	80	6.6	379	2	AAQ06239	AAq06239 sus scrof
123	81.5	6.7	343	2	Q9B4H2	Q9b4h2 cophosaurus	196	80	6.6	406	2	Q6ZC71	Q6zc71 oryza sativ
124	81.5	6.7	347	2	Q6YIV0	Q6yiv0 cophosaurus	197	80	6.6	406	2	BAD09524	Bad09524 oryza sat
125	81.5	6.7	347	2	AAO65533	Aao65533 cophosaur	198	80	6.6	502	2	Q9B973	Q9b973 ceratolen
126	81.5	6.7	453	2	Q7TNK0	Q7tnk0 rattus norv	199	80	6.6	643	2	Q6BSN4	Q6bsn4 debaryomyce
127	81.5	6.7	454	2	Q8AAS4	Q8aas4 bacteroides	200	80	6.6	703	2	Q8VP06	Q8vp06 bruceila ab
128	81.5	6.7	468	2	Q44515	Q44515 caenorhabdi	201	80	6.6	721	2	Q8YG36	Q8yg36 bruceila me
129	81.5	6.7	474	2	Q8EP39	Q8ep39 oceanobacil	202	80	6.6	889	2	Q6ZC72	Q6zc72 oryza sativ
130	81.5	6.7	672	2	Q6G521	Q6g521 bartonella	203	80	6.6	889	2	BAD09523	Bad09523 oryza sat
131	81.5	6.7	1019	2	Q83CM1	Q83cm1 coxiella bu	204	80	6.6	933	2	Q7R539	Q7r539 giardia lam
132	81.5	6.7	1040	2	Q87TN1	Q87tn1 vibrio para	205	80	6.6	1047	2	Q8EBL9	Q8eb19 shewanella
133	81.5	6.7	1687	2	Q6Q117	Q6q117 rattus norv	206	79.5	6.5	154	2	Q9SPW4	Q9spw4 picea glauc
134	81.5	6.7	1687	2	AAS66282	Aas66282 rattus no	207	79.5	6.5	289	2	Q6IUS6	Q6ius6 human herpe
135	81.5	6.7	150	2	Q9SPX8	Q9spX8 picea abies	208	79.5	6.5	341	2	Q8H8E5	Q8hes5 oryza sativ
136	81	6.7	254	1	CHIT PETHY	P29021 petunia hyb	209	79.5	6.5	356	2	Q8LMZ7	Q8lmz7 oryza sativ
137	81	6.7	278	2	Q8KEE7	Q8kee7 chlorobium	210	79.5	6.5	362	2	Q9CNG0	Q9cng0 pasteurella
138	81	6.7	318	2	Q86SG9	Q86sg9 homo sapien	211	79.5	6.5	364	2	Q9LI65	Q9li65 arabidopsis
139	81	6.7	318	2	Q86SH1	Q86sh1 homo sapien	212	79.5	6.5	369	2	Q18053	Q18053 caenorhabdi
140	81	6.7	318	2	Q86SH3	Q86sh3 homo sapien	213	79.5	6.5	390	2	Q7N821	Q7n821 photorhabdu
141	81	6.7	318	2	Q86UG7	Q86ug7 homo sapien	214	79.5	6.5	558	2	Q9M1E2	Q9m1e2 arabidopsis
142	81	6.7	379	2	Q85AW1	Q85aw1 sus scrofa	215	79.5	6.5	608	2	Q8ZND3	Q8zn3 salmoneila
143	81	6.7	379	2	Q8M707	Q8m707 phacochoeru	216	79.5	6.5	654	2	Q7TLW5	Q7tlw5 choristoneu
144	81	6.7	379	2	Q9T568	Q9t568 sus scrofa	217	79.5	6.5	654	2	Q8ZND3	Q8zn3 salmoneila
145	81	6.7	459	2	Q7Y8E6	Q7y8e6 mogera wogu	218	79.5	6.5	654	2	AAp29812	Aap29812 choriston
146	81	6.7	461	2	P91197	P91197 caenorhabdi	219	79.5	6.5	682	2	Q83C62	Q83c62 coxiella bu
147	81	6.7	545	2	Q97TU2	Q97tj2 clostridium	220	79.5	6.5	1143	2	Q9S0B9	Q9s0b9 arabidopsis
148	81	6.7	568	2	Q6BYD1	Q6byd1 debaryomyce	221	79	6.5	289	2	Q9Q0G6	Q9q0g6 human herpe
149	81	6.7	591	2	Q9UI49	Q9ui49 rattus norv	222	79	6.5	379	1	CYB_CAMBA	Cyb36 human bac
150	81	6.7	622	2	Q9C4V0	Q9c4v0 sulfolobus	223	79	6.5	379	1	CYB_CEPCA	Cyb5r1 cephalophus
151	81	6.7	703	2	Q8G1T9	Q8g1t9 bruceila su	224	79	6.5	379	1	CYB_CEPNI	Cyb5r1 cephalophus
152	81	6.7	748	2	Q44416	Q44416 chironomus	225	79	6.5	379	1	CYB_CEPNU	Cyb5r1 cephalophus
153	81	6.7	771	2	Q8A9X0	Q8a9x0 bacteroides	226	79	6.5	379	1	CYB_SUBBA	Q8m703 sus barbatu
154	81	6.7	1038	2	Q6LVZ3	Q6lvz3 photobacter	227	79	6.5	379	2	Q36543	Q36543 sus barbatu
155	81	6.7	1038	2	CAG18532	Cag18532 photobact	228	79	6.5	379	2	Q6GV89	Q6gv89 sus scrofa
156	81	6.7	4226	2	Q8IHY1	Q8ihy1 plasmodium	229	79	6.5	379	2	Q6GV90	Q6gv90 sus scrofa
157	80.5	6.6	205	2	Q6D905	Q6d905 erwinia car	230	79	6.5	379	2	Q6GV91	Q6gv91 sus scrofa
158	80.5	6.6	374	2	Q6FG00	Q6fg00 acinetobact	231	79	6.5	379	2	Q6GV93	Q6gv93 sus scrofa
159	80.5	6.6	379	2	Q9XMB7	Q9xmb7 marmota bai	232	79	6.5	379	2	Q6GV94	Q6gv94 sus scrofa
160	80.5	6.6	395	1	TRFR CHICK	Q93603 gallus gall	233	79	6.5	379	2	Q8HFA8	Q8hf8 camellus bac
161	80.5	6.6	838	2	Q8UTC7	Q8utc7 human immun	234	79	6.5	379	2	Q8M702	Q8m702 sus barbatu
162	80.5	6.6	878	2	Q8EW47	Q8ew47 mycoplasma	235	79	6.5	379	2	Q9B5R9	Q9b5r9 cephalophus
163	80	6.6	140	2	Q85PI7	Q85p17 sus scrofa	236	79	6.5	379	2	AAm95581	Aam95581 camellus b
164	80	6.6	314	2	Q924X8	Q924x8 mus musculu	237	79	6.5	379	2	AAm95583	Aam95583 camellus b
165	80	6.6	324	2	Q7S346	Q7s346 neurospora	238	79	6.5	379	2	AAm95584	Aam95584 camellus b
166	80	6.6	352	1	OPSD GOBNI	Q9ygz2 gobius nige	239	79	6.5	468	2	AAm95585	Aam95585 camellus b
167	80	6.6	352	1	Q9PRU8	Q9prj8 xenopus lae	240	79	6.5	468	2	Q7VFP4	Q7vfp4 heliobacte
168	80	6.6	356	2	Q9GCS0	Q9gcs0 petinomys s	241	79	6.5	595	2	Q6YK44	Q6yk44 oryza sativ
169	80	6.6	356	2	Q9GCSI	Q9gcsi hyloupetes p	242	79	6.5	595	2	Q84KR4	Q84kr4 oryza sativ
170	80	6.6	379	1	CYB_PIG	P24964 sus scrofa	243	79	6.5	595	2	AAm15219	Aam15219 oryza sat
171	80	6.6	379	1	Q71KJ5	Q71kj5 sus scrofa	244	79	6.5	787	2	Q80V13	Q80v13 mus musculu
172	80	6.6	379	2	Q6GV86	Q6gv86 sus scrofa	245	79	6.5	1052	2	Q89F84	Q89f84 bradyrhizob
173	80	6.6	379	2	Q85QJ9	Q85qj9 sus scrofa	246	79	6.5	1353	1	CYA9 MOUSE	Cya9 mouse mus musculu
174	80	6.6	379	2	Q9T4J0	Q9t4j0 sus scrofa	247	78.5	6.5	208	2	Q7M8B1	Q7m8b1 wolinnella s
175	80	6.6	379	2	Q9T565	Q9t565 sus scrofa	248	78.5	6.5	240	2	Q6P7J5	Q6p7j5 xenopus lae
176	80	6.6	379	2	Q9T566	Q9t566 sus scrofa	249	78.5	6.5	240	2	AAH61648	Aah61648 xenopus l
177	80	6.6	379	2	Q9T567	Q9t567 sus scrofa	250	78.5	6.5	276	2	Q9WNS8	Q9wns8 human herpe

251	78.5	6.5	289	2	Q9WHC1	Q9whc1 human herpe	324	77.5	6.4	500	2	O51549	O51549 borrelia bu
252	78.5	6.5	322	2	Q18269	Q18269 caenorhabdi	325	77.5	6.4	557	2	P94622	P94622 clostridium
253	78.5	6.5	328	2	O88775	O88775 rattus norv	326	77.5	6.4	565	2	O8A4R9	O8a4r9 bacteroides
254	78.5	6.5	328	2	AAH61846	Aah61846 rattus no	327	77.5	6.4	825	2	O9FK21	O9fk21 arabidopsis
255	78.5	6.5	363	2	O7CYI6	O7cyi6 agrobacteri	328	77.5	6.4	1107	2	O76NT1	O76nt1 dictyosteli
256	78.5	6.5	363	2	O8UEG6	O8ueg6 agrobacteri	329	77.5	6.4	1107	2	AAS38831	Aas38831 dictyoste
257	78.5	6.5	423	2	O9FH91	O9fhn1 arabidopsis	330	77	6.3	309	2	O8CTN3	O8ctn3 staphylococ
258	78.5	6.5	452	2	Q8WFA0	Q8wfa0 venerupis (	331	77	6.3	314	2	O6ZAX4	O6zax4 oryza sativ
259	78.5	6.5	648	2	Q76L35	Q76l35 nicotiana t	332	77	6.3	314	2	BAC99611	Bac99611 platyneris
260	78.5	6.5	648	2	BAC23059	Bac23059 nicotiana	333	77	6.3	328	2	O9TB46	O9tb46 platyneris
261	78.5	6.5	760	1	AD25 MOUSE	Q9r159 mus musculu	334	77	6.3	379	2	Q9MNV4	Q9mnv4 martes amer
262	78.5	6.5	1039	2	O7MOH1	Q7mqh1 vibrio vuln	335	77	6.3	379	2	Q9B5Q9	Q9b5q9 cephalophus
263	78.5	6.5	1039	2	Q8DDC6	Q8ddc6 vibrio vuln	336	77	6.3	379	2	O9G4V1	O9g4v1 martes amer
264	78	6.4	227	2	O74HY8	Q74hy8 lactobacill	337	77	6.3	379	2	Q9G7S6	Q9g7s6 sus scrofa
265	78	6.4	227	2	AAS09552	Aae09552 lactobaci	338	77	6.3	379	2	Q8WBM1	Q8wbm1 martes amer
266	78	6.4	285	2	Q92LL3	Q92ll3 rhizobium m	339	77	6.3	424	2	O6D859	Q6d859 erwina car
267	78	6.4	297	2	O8NXT3	Q8nxt3 staphylococ	340	77	6.3	452	2	O6BQ77	Q6bq77 debaryomyce
268	78	6.4	309	2	O6GBL1	Q6gb11 staphylococ	341	77	6.3	471	2	O85YM1	Q85ym1 monadenium
269	78	6.4	309	2	Q99VZ6	Q99vz6 staphylococ	342	77	6.3	516	2	O9B5Z5	Q9b5z5 pseudostylo
270	78	6.4	309	2	O7A731	Q7a731 staphylococ	343	77	6.3	534	2	O8RWH6	Q8rwh6 arabidopsis
271	78	6.4	329	2	O76BK6	Q76bk6 paralichthy	344	77	6.3	537	2	O7S496	Q7s496 neurospora
272	78	6.4	329	2	BAD02483	Bad02483 paralicht	345	77	6.3	577	2	O85QO7	Q85qg7 gomphioceph
273	78	6.4	356	2	Q8WFE3	Q8wfe3 petaurista	346	77	6.3	581	2	PRLR SHEEP	O46561 ovis aries
274	78	6.4	379	1	CYB_CEPHE	Q9tcl4 cephalorhyn	347	77	6.3	590	2	O9STC7	O9stc7 dunaliella
275	78	6.4	379	1	CYB_PHAAE	Q8m708 phacochoeu	348	77	6.3	677	2	O7Q5S8	Q7q6s8 giardia lam
276	78	6.4	379	2	O8M709	Q8m709 phacochoeu	349	77	6.3	1032	1	Y895 HAEIN	Q7q6s8 giardia lam
277	78	6.4	379	2	Q9XMC0	Q9xmc0 marmota cau	350	77	6.3	1061	2	Q986H1	Q986h1 haemophilus
278	78	6.4	379	2	O92LI18	Q92li18 rhizobium m	351	77	6.3	1188	2	O7RMN3	Q7rmn3 neurospora
279	78	6.4	380	2	O7Y752	Q7y752 zoogoneticu	352	77	6.3	1215	2	P93750	P93750 arabidopsis
280	78	6.4	380	2	O7YHK2	Q7yhk2 zoogoneticu	353	77	6.3	2651	2	O8IAV6	Q8iav6 plasmodium
281	78	6.4	409	2	O73GC5	Q73gc5 wolbachia p	354	77	6.3	222	2	O7B5K3	Q7b5k3 lactobacill
282	78	6.4	409	2	AAS14691	Aas14691 wolbachia	355	76.5	6.3	222	2	AAS21881	Aas21881 lactobaci
283	78	6.4	457	2	O8A565	O8a565 bacteroides	356	76.5	6.3	232	2	O6MG59	Q6mg59 rattus norv
284	78	6.4	519	2	O6CXK7	Q6cxk7 kluyveromyc	357	76.5	6.3	232	2	CAB83987	Caeb3987 rattus no
285	78	6.4	555	2	O869R1	Q869r1 dictyosteli	358	76.5	6.3	248	2	O7QYX9	Q7qyx9 giardia lam
286	78	6.4	641	2	O7ZZM2	Q7zzw2 paralichthy	359	76.5	6.3	268	2	O6XFAL	Q6xfal psammophis
287	78	6.4	717	2	O7XKF4	Q7xkf4 oryza sativ	360	76.5	6.3	274	2	Q995B5	Aap78955 psammophi
288	78	6.4	832	2	O8IBT8	Q8ibc8 plasmodium	361	76.5	6.3	289	2	O80IF2	Q80if2 human herpe
289	78	6.4	899	2	O6FP46	Q6fp46 candida gla	362	76.5	6.3	289	2	Q995B5	Q995b5 human herpe
290	78	6.4	1059	2	Q88HD4	Q88hd4 pseudomonas	363	76.5	6.3	289	2	O80IF2	Q80if2 human herpe
291	78	6.4	1062	2	P95422	P95422 pseudomonas	364	76.5	6.3	333	2	O8KVY0	Q8kvy0 ruegeria sp
292	78	6.4	1062	2	Q9IOY8	Q9ioy8 pseudomonas	365	76.5	6.3	343	2	Q859X2	Q859x2 uma exsul.
293	78	6.4	1280	2	Q86JR7	Q86jr7 dictyosteli	366	76.5	6.3	343	2	O85KP0	Q85kp0 uma exsul.
294	78	6.4	1783	2	Q18698	Q18698 caenorhabdi	367	76.5	6.3	377	2	O8KOP5	Q8kop5 mus musculu
295	78	6.4	1877	2	Q8MQA1	Q8mqa1 caenorhabdi	368	76.5	6.3	379	1	CYB_CANFA	Q34101 canis fami1
296	77.5	6.4	151	2	Q9SPX9	Q9spx9 picea abies	369	76.5	6.3	379	1	CYB_MARMA	Q9xp34 marmota mar
297	77.5	6.4	218	2	Q932K2	Q932k2 staphylococ	370	76.5	6.3	379	2	O6JWX7	Q6jwx7 canis aureu
298	77.5	6.4	274	2	Q995A5	Q995a5 human herpe	371	76.5	6.3	379	2	O6Y8J2	O6y8j2 canis lupus
299	77.5	6.4	320	2	O6D431	Q6d431 erwina car	372	76.5	6.3	379	2	Q9G3M7	Q9g3m7 rhizomys si
300	77.5	6.4	343	2	Q9B4H0	Q9b4h0 callisaurus	373	76.5	6.3	379	2	BAB39140	Bab39140 canis fam
301	77.5	6.4	347	2	O6YIU5	O6yiu5 callisaurus	374	76.5	6.3	379	2	AAQ56603	Aaq56603 canis lup
302	77.5	6.4	379	1	AAO65538	Aao65538 callisaur	375	76.5	6.3	379	2	AAQ56601	Aaq56601 canis lup
303	77.5	6.4	379	2	CYB_LAMVI	Q9tcl3 marmota cau	376	76.5	6.3	379	2	AAQ56603	Aaq56603 canis aur
304	77.5	6.4	379	2	Q9T3R3	Q9t3r3 marmota cau	377	76.5	6.3	379	2	AAQ56601	Aaq56601 canis lup
305	77.5	6.4	379	2	Q9TF94	Q9tf94 spermophilu	378	76.5	6.3	426	2	Q9W3R5	Q9w3r5 drosophila
306	77.5	6.4	379	2	Q9TF95	Q9tf95 spermophilu	379	76.5	6.3	451	2	O69657	O69657 mycobacteri
307	77.5	6.4	379	2	O8W9E4	Q8w9e4 sciurus aes	380	76.5	6.3	451	2	O7TVX6	O7tvx6 mycobacteri
308	77.5	6.4	434	2	Q6NFEZ8	Q6nfez corynebacte	381	76.5	6.3	451	2	O7TVX6	O7tvx6 mycobacteri
309	77.5	6.4	434	2	CAE50266	Caes0266 corynebac	382	76.5	6.3	538	2	Q9MLT4	Q9mlt4 arabidopsis
310	77.5	6.4	437	2	O7WR18	Q7wr18 staphylococ	383	76.5	6.3	556	2	O6BVD3	Q6bvd3 debaryomyce
311	77.5	6.4	452	2	O7YF45	Q7yf45 venerupis (	384	76.5	6.3	557	2	O6FLC9	Q6flc9 candida gla
312	77.5	6.4	452	2	O7YF47	Q7yf47 venerupis (	385	76.5	6.3	557	2	O7KVU5	Q7kvu5 drosophila
313	77.5	6.4	452	2	O7YF50	Q7yf50 venerupis (	386	76.5	6.3	557	2	AAS65269	Aas65269 drosophi1
314	77.5	6.4	452	2	O7YF51	Q7yf51 venerupis (	387	76.5	6.3	574	2	Q9TWI3	Q9twi3 leishmania
315	77.5	6.4	452	2	O7YF52	Q7yf52 venerupis (	388	76.5	6.3	598	2	O9ULG0	O9ulg0 leishmania
316	77.5	6.4	453	1	TDE2_MOUSE	Q9qzi8 mus musculu	389	76.5	6.3	614	1	DNAX_ODOSI	Dnax0dos1 odontella b
317	77.5	6.4	456	2	O6BO78	Q6bq78 debaryomyce	390	76.5	6.3	722	2	O9FOW5	Q9fow5 pseudomonas
318	77.5	6.4	459	1	NU4M_RABIT	Q79436 oryctolagus	391	76	6.3	141	2	O47929	O47929 exoneura tr
319	77.5	6.4	459	2	O6GCC4	Q6gcc4 staphylococ	392	76	6.3	249	2	O7R5F7	O7r5f7 giardia lam
320	77.5	6.4	459	2	O6GK94	Q6gk94 staphylococ	393	76	6.3	289	1	OPSD_COMDY	O42327 comephorus
321	77.5	6.4	459	2	O99X01	O99x01 staphylococ	394	76	6.3	310	2	O8VG54	O8vg54 mus musculu
322	77.5	6.4	459	2	O7A1X0	Q7a1x0 staphylococ	395	76	6.3	312	2	O8TKV9	O8tkv9 methanosarc
323	77.5	6.4	494	2	O87S84	Q87s84 vibrio para	396	76	6.3	330	2	O85T18	O85t18 anolis roqu

397	76	6.3	343	2	Q85KP4	Q85kp4 uma exsul.	470	75.5	6.2	409	1	MNTH_YERPE	Q8zck2 yersinia pe
398	76	6.3	346	2	O16913	O16913 caenorthabdi	471	75.5	6.2	431	2	Q9s333	Q9s333 prochloroco
399	76	6.3	379	1	CYB_MARME	Q9t3h9 martes mela	472	75.5	6.2	431	2	Q7BW18	Q7bw18 prochloroco
400	76	6.3	379	1	CYB_PTEHP	Q8s1z4 pteropus hy	473	75.5	6.2	476	2	Q9s1A5	Q9s1a5 arabidopsis
401	76	6.3	379	2	Q78726	Q78726 sus scrofa	474	75.5	6.2	494	2	Q7MNM2	Q7mn2 vibrio vuln
402	76	6.3	379	2	Q71120	Q71120 martes zibe	475	75.5	6.2	494	2	Q8DEF3	Q8de3 vibrio vuln
403	76	6.3	379	2	Q8M700	Q8m700 sus verruco	476	75.5	6.2	578	2	Q85U12	Q85u12 ciona bavig
404	76	6.3	379	2	Q8M701	Q8m701 sus verruco	477	75.5	6.2	593	2	Q6BM61	Q6bm61 debaryomyce
405	76	6.3	379	2	Q9T7P0	Q9t7p0 tachyocycte	478	75.5	6.2	609	2	Q88F25	Q88f25 pseudomonas
406	76	6.3	379	2	Q9B5R7	Q9b5r7 cephalophus	479	75.5	6.2	788	1	QOXM_SULAC	Q394f1 sulfolobus
407	76	6.3	379	2	Q9GBH0	Q9gbh0 martes mart	480	75.5	6.2	824	2	Q40713	Q40713 oryza sativ
408	76	6.3	379	2	Q9GBH3	Q9gbh3 martes amer	481	75.5	6.2	849	2	Q8T3V2	Q8t3v2 drosophila
409	76	6.3	379	2	Q8WBM0	Q8w7d6 martes mart	482	75.5	6.2	864	2	Q6BGY9	Q6bgy9 debaryomyce
410	76	6.3	380	2	Q7YE34	Q8wbm0 martes zibe	483	75.5	6.2	886	2	Q8KAY9	Q8kay9 chlorobium
411	76	6.3	380	2	Q7YHK3	Q7ye34 microspatho	484	75.5	6.2	1099	2	Q18633	Q18633 caenorthabdi
412	76	6.3	380	2	Q6L2S9	Q7yhk3 zoogoneticu	485	75.5	6.2	1099	2	CAA99786	Caa99786 caenorhab
413	76	6.3	405	2	Q6L2S9	Q6l2s9 picrophilus	486	75.5	6.2	1173	2	Q6NR54	Q6nr54 drosophila
414	76	6.3	410	2	Q9XP09	Q9xp09 parapantetele	487	75.5	6.2	1173	2	AAQ23543	Aaq23543 drosophil
415	76	6.3	430	2	Q6Y0P9	Q6y0p9 staphylococ	488	75.5	6.2	1683	2	Q86KY1	Q86ky1 dictyosteli
416	76	6.3	430	2	AAp32320	AAp32320 staphyloc	489	75.5	6.2	1683	2	AAO50849	Aao50849 dictyoste
417	76	6.3	431	2	Q6LMG4	Q6lmg4 lactobacill	490	75.5	6.2	4226	2	Q9N9H5	Q9n9h5 plasmodium
418	76	6.3	431	2	Q8Y7H9	Q8y7h9 listeria mo	491	75	6.2	111	2	Q9XEF7	Q9xe7 arabidopsis
419	76	6.3	431	2	CAG17844	Q76l72 euphausia s	492	75	6.2	176	2	Q8TIK1	Q8tik1 methanosarc
420	76	6.3	445	2	Q76L72	Q76l72 euphausia s	493	75	6.2	253	2	Q8AW18	Q8aw18 chloroscomb
421	76	6.3	445	2	BAD16768	Bad16768 euphausia	494	75	6.2	299	2	Q8AWR5	Q8awr5 brachydanio
422	76	6.3	447	2	Q6G7E5	Q6g7e5 staphylococ	495	75	6.2	312	2	Q6MFX2	Q6mfx2 rattus norv
423	76	6.3	447	2	Q8VUH5	Q8vuh5 staphylococ	496	75	6.2	312	2	CAE84075	CaE84075 rattus no
424	76	6.3	447	2	Q8NVE0	Q8nve0 staphylococ	497	75	6.2	330	2	Q8ST15	Q8st15 anolis roqu
425	76	6.3	447	2	Q9S9S97	Q9s9s97 staphylococ	498	75	6.2	330	2	Q8ST16	Q8st16 anolis roqu
426	76	6.3	453	2	Q6UKF6	Q6ukf6 phoronis ps	499	75	6.2	347	2	Q6Y1W1	Q6yiv1 phrynosoma
427	76	6.3	453	2	AAr13394	AAr13394 phoronis	500	75	6.2	347	2	AAO65522	Aao65522 phrynosom
428	76	6.3	505	2	Q972X7	Q972x7 sulfolobus	501	75	6.2	360	2	Q8HIC0	Q8hic0 callosciuru
429	76	6.3	515	2	Q8BGA3	Q8bga3 m mus muscu	502	75	6.2	373	2	Q8Z089	Q8z089 anabaena sp
430	76	6.3	515	2	Q8C8L1	Q8c8l1 mus musculu	503	75	6.2	379	1	CYB_CEPNG	Q9b5r0 cephalophus
431	76	6.3	528	2	Q80U08	Q80u08 mus musculu	504	75	6.2	379	1	CYB_GULGU	P56697 guilo guilo (
432	76	6.3	532	1	YHCA_BACSU	P54585 bacillus su	505	75	6.2	379	1	CYB_MESH1	Q35000 mesomys his
433	76	6.3	543	2	Q9DX16	Q9dxy6 avian infec	506	75	6.2	379	2	Q99341	Q99341 aepyrocero m
434	76	6.3	559	2	Q7QR36	Q7qr36 giardia lam	507	75	6.2	379	2	P92579	P92579 bubalus dep
435	76	6.3	561	2	O17947	O17947 caenorthabdi	508	75	6.2	379	2	P92867	P92867 bubalus dep
436	76	6.3	604	2	Q93700	Q93700 sulfolobus	509	75	6.2	379	2	Q7G104	Q7g104 mesomys his
437	76	6.3	742	2	Q23766	Q23766 chironomus	510	75	6.2	379	2	Q71YN8	Q71yn8 cephalophus
438	76	6.3	751	2	O01835	O01835 caenorthabdi	511	75	6.2	379	2	Q8HBR1	Q8hbr1 camelus bac
439	76	6.3	814	2	Q9VNP2	Q9vnp2 drosophila	512	75	6.2	379	2	Q8HFA7	Q8hfa7 camelus bac
440	76	6.3	814	2	AAf51887	Aaf51887 drosophil	513	75	6.2	379	2	Q9XK52	Q9xk52 marmota sib
441	76	6.3	981	2	Q7Q074	Q7q074 anopheles g	514	75	6.2	379	2	Q9XLD8	Q9xld8 kobus ellip
442	76	6.3	1011	2	Q24273	Q24273 drosophila	515	75	6.2	379	2	Q9XLD9	Q9xld9 kobus ellip
443	76	6.3	1043	2	Q6LNM7	Q6lmn7 photobacter	516	75	6.2	379	2	Q9B1D2	Q9b1d2 cephalophus
444	76	6.3	1043	2	CAG21099	Cag21099 photobact	517	75	6.2	379	2	Q9B5Q3	Q9b5q3 cephalophus
445	75.5	6.2	111	2	Q90X36	Q90x36 brachydanio	518	75	6.2	379	2	Q9B5R6	Q9b5r6 cephalophus
446	75.5	6.2	138	2	P71459	P71459 lactobacill	519	75	6.2	379	2	Q9B5S1	Q9b5s1 cephalophus
447	75.5	6.2	142	2	Q8HMM9	Q8hmm9 allodape mu	520	75	6.2	380	2	Q7YEF3	Q7ye73 chromis xan
448	75.5	6.2	151	2	Q9SPW5	Q9spw5 picea glauc	521	75	6.2	380	2	Q9T578	Q9t578 acornys sp.
449	75.5	6.2	222	2	Q88ZC6	Q88zc6 lactobacill	522	75	6.2	385	2	Q9PFR8	Q9pfr8 xylella fas
450	75.5	6.2	239	2	Q75QB4	Q75qb4 human coxsa	523	75	6.2	396	2	Q8D2O7	Q8d2q7 wiggleswort
451	75.5	6.2	239	2	Q6DCQ3	Q6dcq3 xenopus lae	524	75	6.2	452	2	Q6GMG6	Q6gmj6 brachydanio
452	75.5	6.2	239	2	BAD11163	Bad11163 human cox	525	75	6.2	452	2	Q6RI96	Q6ri96 rhizobium f
453	75.5	6.2	275	2	Q6GIG5	Q6g195 staphylococ	526	75	6.2	519	2	AAr91685	Aar91685 rhizobium
454	75.5	6.2	343	2	Q8SCB0	Q8scb0 uma exsul.	527	75	6.2	527	2	Q8XU76	Q8xu76 enterococcu
455	75.5	6.2	343	2	Q8SKP1	Q8skp1 uma exsul.	528	75	6.2	566	2	Q73YMO	Q73ymo mycobacteri
456	75.5	6.2	347	2	Q6YIU9	Q6yiu9 holbrookia	529	75	6.2	566	2	AA504252	Aa504252 mycobacte
457	75.5	6.2	347	2	AAO65534	Aao65534 holbrooki	530	75	6.2	570	2	Q9B510	Q9b510 tetrodontop
458	75.5	6.2	348	2	Q8MQU1	Q8mqul paracentrot	531	75	6.2	581	1	PRLR_BOVIN	Q28172 bos taurus
459	75.5	6.2	364	2	Q92PR2	Q92pr2 rhizobium m	532	75	6.2	726	2	Q6CTB9	Q6ctb9 yarrowia li
460	75.5	6.2	378	2	Q70EH3	Q70eh3 saccostomus	533	75	6.2	853	2	Q93245	Q93245 oncorhynchu
461	75.5	6.2	378	2	CAE48144	CaE48144 saccostom	534	75	6.2	1015	2	Q09938	Q09938 caenorthabdi
462	75.5	6.2	379	2	O20611	O20611 coetomys da	535	75	6.2	2201	1	TENA_HUMAN	P24821 homo sapien
463	75.5	6.2	379	2	O21789	O21789 ctenomys fr	536	74.5	6.1	146	2	Q8LXC1	Q8lxc1 martes amer
464	75.5	6.2	379	2	Q6T8R4	Q6t8r4 spermophilu	537	74.5	6.1	202	2	Q6ZV01	Q6zv01 homo sapien
465	75.5	6.2	379	2	Q9XP28	Q9xp28 marmota cal	538	74.5	6.1	202	2	BAC86065	Bac85065 homo sapi
466	75.5	6.2	379	2	Q9GBG7	Q9gbg7 guilo guilo (	539	74.5	6.1	239	2	Q8BJU2	Q8bjuz mus musculu
467	75.5	6.2	379	2	AAr88275	Aar88275 spermophi	540	74.5	6.1	246	2	Q9MF63	Q9mf63 beta vulgar
468	75.5	6.2	380	2	Q94SX5	Q94sx5 cololabis s	541	74.5	6.1	265	2	Q896Z5	Q896z5 clostridium
469	75.5	6.2	384	2	Q37623	Q37623 prototheca	542	74.5	6.1	268	2	Q6NIZ8	Q6ni28 corynebacte



543	74.5	6.1	268	2	CAE49135	Ca649135 coryneb	616	74	6.1	379	2	O99339	O99339 neotragus m
544	74.5	6.1	289	2	O93938	O93938 saccharomyc	617	74	6.1	379	2	O7Y8L5	O7Y8L5 myotis form
545	74.5	6.1	289	2	O9WHC9	O9whc9 human herpe	618	74	6.1	379	2	O33948	O33948 bubalus bub
546	74.5	6.1	296	2	O722C5	O722c5 listeria mo	619	74	6.1	379	2	O35087	O35087 mesomys sp.
547	74.5	6.1	296	2	AAT03589	Aat03589 listeria	620	74	6.1	379	2	O35093	O35093 mesomys sp.
548	74.5	6.1	310	2	O7V7B4	O7v7b4 prochloroco	621	74	6.1	379	2	O66V88	O66v88 sus scrofa
549	74.5	6.1	318	2	O970J0	O970j0 sulfolobus	622	74	6.1	379	2	O8HB83	O8hb83 camelus dro
550	74.5	6.1	328	2	O6JP46	O6jp46 radula comp	623	74	6.1	379	2	O9TF64	O9tf64 spermophilu
551	74.5	6.1	330	2	O85T11	O85t11 anolis roqu	624	74	6.1	379	2	O9TH47	O9th47 marmota cal
552	74.5	6.1	332	2	O82XG2	O82xg2 pyrobaculum	625	74	6.1	379	2	O9B5R4	O9b5r4 cephalophus
553	74.5	6.1	343	2	O85CS6	O85cs6 uma paraphy	626	74	6.1	379	2	O94ND7	O94nd7 ctenomys tu
554	74.5	6.1	343	2	O85KN5	O85kn5 uma paraphy	627	74	6.1	379	2	O94PB4	O94pb4 tamias amoe
555	74.5	6.1	343	2	O85KN6	O85kn6 uma paraphy	628	74	6.1	379	2	O94WY4	O94wy4 ctenomys tu
556	74.5	6.1	343	2	O85KN8	O85kn8 uma paraphy	629	74	6.1	379	2	O8W9L6	O8w9l6 glaucomys v
557	74.5	6.1	343	2	O85KN9	O85kn9 uma paraphy	630	74	6.1	385	2	O87B96	O87b96 xylella fas
558	74.5	6.1	343	2	O85KP2	O85kp2 uma exsul.	631	74	6.1	405	2	O69757	O69757 pseudomonas
559	74.5	6.1	346	2	O9GCS2	O9gcs2 tamiasciuru	632	74	6.1	410	2	O6E8J0	O6e8j0 heteronotus
560	74.5	6.1	376	2	O9TH54	O9th54 marmota mon	633	74	6.1	430	2	O6YON7	O6yon7 staphylococ
561	74.5	6.1	377	2	O93F46	O93f46 edwardsiell	634	74	6.1	430	2	AAP32332	Aap32332 staphyloc
562	74.5	6.1	378	2	O94Y65	O94y65 tamiasciuru	635	74	6.1	431	2	O92C53	O92c53 listeria in
563	74.5	6.1	378	2	O8NLI3	O8nl13 corynebacte	636	74	6.1	448	2	O6P9E0	O6p9e0 homo sapien
564	74.5	6.1	379	1	CYB_AMMHA	O9tf30 ammospemop	637	74	6.1	448	2	O86UT0	O86ut0 homo sapien
565	74.5	6.1	379	1	CYB_CTECO	O21764 ctenomys co	638	74	6.1	448	2	O9NWP4	O9nwf4 homo sapien
566	74.5	6.1	379	2	O347I17	O347i17 hippotragus	639	74	6.1	448	2	AAB60810	Aab60810 homo sapl
567	74.5	6.1	379	2	O9TH46	O9th46 marmota bro	640	74	6.1	476	2	O7Q579	O7q579 anopheles g
568	74.5	6.1	379	2	O9XMB8	O9xmb8 marmota bro	641	74	6.1	485	2	O7VSU8	O7vsu8 bordetella
569	74.5	6.1	379	2	O9B9F5	O9b9f5 chrotogale	642	74	6.1	485	2	O7WFS9	O7wfs9 bordetella
570	74.5	6.1	379	2	AAG60335	Aag60335 chrotogal	643	74	6.1	501	2	O6GIR4	O6gir4 staphylococ
571	74.5	6.1	407	2	O6MDT1	O6mdt1 parachlamyd	644	74	6.1	505	2	O82SC4	O82sc4 nitrosomona
572	74.5	6.1	407	2	CAF23268	Caf23268 parachlam	645	74	6.1	528	2	O9B981	O9b981 blastophaga
573	74.5	6.1	410	2	O6E822	O6e822 umbonia ata	646	74	6.1	555	2	O9M171	O9m171 arabidopsis
574	74.5	6.1	416	2	O6M1T5	O6m1t5 corynebacte	647	74	6.1	602	2	O6C4W0	O6c4w0 yarowia li
575	74.5	6.1	416	2	CAF20953	Caf20953 corynebac	648	74	6.1	687	2	O8W3M2	O8w3m2 citrus unsh
576	74.5	6.1	428	2	O7P9H7	O7p9h7 rickettsia	649	74	6.1	713	2	O6CPC7	O6cpc7 kluyveromyc
577	74.5	6.1	429	1	ARSB_STAXY	O01255 staphylococ	650	74	6.1	756	2	O7M762	O7m762 mus musculu
578	74.5	6.1	432	1	RMUC_RICCN	O92gr5 rickettsia	651	74	6.1	826	2	O7TSL4	O7t8l4 rattus norv
579	74.5	6.1	453	2	O7V4H7	O7v4h7 prochloroco	652	74	6.1	857	2	O91XN5	O91xn5 rattus norv
580	74.5	6.1	458	1	TCR_STAHY	O91q76 arabidopsis	653	74	6.1	1873	2	O83044	O83044 lettuce inf
581	74.5	6.1	462	2	O6GQP2	O6gqp2 staphylococ	654	73.5	6.0	140	2	O9XMB1	O9xmb1 palorus gen
582	74.5	6.1	468	2	O9KUT2	O9kut2 vibrio chol	655	73.5	6.0	142	2	O8HMP6	O8hmp6 compsomelis
583	74.5	6.1	473	2	O9W1Y9	O9w1y9 drosophila	656	73.5	6.0	191	2	O8HKK7	O8hkk7 allodape sk
584	74.5	6.1	518	2	O83MI2	O83mi2 tropheryma	657	73.5	6.0	243	2	O8ELD6	O8eld6 oceanobacil
585	74.5	6.1	518	2	O83MP0	O83mp0 tropheryma	658	73.5	6.0	250	2	O8WEL5	O8wel5 pogonomyrme
586	74.5	6.1	522	2	O8JRR2	O8jrr2 phtorimaea	659	73.5	6.0	250	2	O81WR6	O81wr6 bacillus an
587	74.5	6.1	559	2	O8JRR34	O8jrr34 avian infec	660	73.5	6.0	257	2	AAT33015	Aat33015 bacillus
588	74.5	6.1	618	2	O9ZTZ7	O9ztc27 arabidopsis	661	73.5	6.0	257	2	O23189	O23189 caenorhabdi
589	74.5	6.1	618	2	O9LQ76	O9lq76 arabidopsis	662	73.5	6.0	261	1	CLDI_HUMAN	P56856 homo sapien
590	74.5	6.1	641	2	O88E58	O88e58 pseudomonas	663	73.5	6.0	347	2	O6YIV8	O6yiv8 phrynosoma
591	74.5	6.1	677	2	O77LV0	O77lv0 helicoverpa	664	73.5	6.0	347	2	O6YIV9	O6yiv9 phrynosoma
592	74.5	6.1	677	2	O99GS9	O99gs9 helicoverpa	665	73.5	6.0	347	2	AAO65524	Aao65524 phrynosom
593	74.5	6.1	729	2	O85FH9	O85fh9 adiantum ca	666	73.5	6.0	347	2	AAO65525	Aao65525 phrynosom
594	74.5	6.1	740	2	O6NNU5	O6nnu5 brachydanio	667	73.5	6.0	350	2	O6BNJ6	O6bnj6 debaryomyc
595	74.5	6.1	740	2	AAH68425	Aah68425 brachydan	668	73.5	6.0	353	2	O9PT68	O9pt68 xenopus lae
596	74.5	6.1	763	2	O81IQ4	O81iq4 mus musculu	669	73.5	6.0	360	2	O6BMS1	O6bms1 debaryomyc
597	74.5	6.1	1054	2	O75HC2	O75hc2 oryza sativ	670	73.5	6.0	373	2	O8CU33	O8cu33 staphylococ
598	74.5	6.1	1054	2	AAS01930	Aas01930 oryza sat	671	73.5	6.0	379	1	CYB_ASTPE	O33818 asterina pe
599	74.5	6.1	1059	2	O8JHB1	O8jhb1 squalus aca	672	73.5	6.0	379	1	CYB_GLASA	O48372 glaucomyx s
600	74.5	6.1	1059	2	O8JHB3	O8jhb3 squalus aca	673	73.5	6.0	379	1	CYB_TRASR	O9c9b7 tragalaphus
601	74.5	6.1	1062	2	O89NG9	O89ng9 bradyrhizob	674	73.5	6.0	379	2	O20613	O20613 cryptomys c
602	74.5	6.1	1091	2	O8JHB5	O8jhb5 squalus aca	675	73.5	6.0	379	2	O6T8R1	O6t8r1 spermophilu
603	74.5	6.1	1709	1	SN_HUMAN	O9bzz2 homo sapien	676	73.5	6.0	379	2	O9TF05	O9tf05 marmota mon
604	74	6.1	114	2	O8X1T9	O8x1t9 pholiota na	677	73.5	6.0	379	2	O9TF65	O9tf65 spermophilu
605	74	6.1	140	2	O85PI9	O85pi9 canis famil	678	73.5	6.0	379	2	O9TF67	O9tf67 spermophilu
606	74	6.1	268	2	O822A6	O822a6 chlamydophi	679	73.5	6.0	379	2	O9TH53	O9th53 marmota mon
607	74	6.1	282	2	O9PUZ5	O9puz5 balistes sp	680	73.5	6.0	379	2	O9TH55	O9th55 marmota mon
608	74	6.1	307	2	O7TRS1	O7tr51 mus musculu	681	73.5	6.0	379	2	O94WX4	O94wx4 ctenomys au
609	74	6.1	307	2	AAP71539	Aap71539 mus muscu	682	73.5	6.0	379	2	AAR88278	Aar88278 spermophi
610	74	6.1	330	2	O85T09	O85t09 anolis roqu	683	73.5	6.0	387	2	O9SIC2	O9sic2 arabidopsis
611	74	6.1	330	2	O85T21	O85t21 anolis roqu	684	73.5	6.0	428	2	O83E21	O83e21 coxiella bu
612	74	6.1	369	2	O70VE5	O70ve5 sorex minut	685	73.5	6.0	429	1	ARSB_STAUA	P30329 staphylococ
613	74	6.1	369	2	CAD59514	Cad59514 sorex min	686	73.5	6.0	429	2	O9AC73	O9ac73 staphylococ
614	74	6.1	379	1	CYB_CAMDR	P24952 camelus dro	687	73.5	6.0	459	2	O955S3	O955s3 microcebus
615	74	6.1	379	1	CYB_KOBEL	O99342 kobus ellip	688	73.5	6.0	463	2	O6HNC2	O6hnc2 bacillus th

689	73.5	6.0	477	2	Q7WCB2	Q7wcb2 bordetella	762	73	6.0	379	2	Q9XP69	Q9xp69 cephalophus
690	73.5	6.0	507	2	Q978U2	Q978u2 thermoplasm	763	73	6.0	379	2	Q9WT63	Q9wm63 plataniesta
691	73.5	6.0	544	2	Q97M46	Q97m46 clostridium	764	73	6.0	379	2	Q9B5Q2	Q9b5c2 sylvicapra
692	73.5	6.0	593	2	Q8W104	Q8w104 arabidopsis	765	73	6.0	379	2	Q9B5Q4	Q9b5c4 cephalophus
693	73.5	6.0	640	2	Q88QU0	Q88qu0 pseudomonas	766	73	6.0	379	2	Q9B5Q5	Q9b5c5 cephalophus
694	73.5	6.0	644	1	CD93_MOUSE	Q89103 mus musculu	767	73	6.0	379	2	Q9B5Q7	Q9b5c7 cephalophus
695	73.5	6.0	644	2	BAC37518	Bac37518 mus muscu	768	73	6.0	379	2	Q9B5S0	Q9b5e0 cephalophus
696	73.5	6.0	654	2	Q8EUQ4	Q8euq4 mycoplasma	769	73	6.0	379	2	Q9G3N7	Q9g3r7 eospalax fo
697	73.5	6.0	720	2	Q6YXQ6	Q6yxq6 physcomitre	770	73	6.0	379	2	Q94PT4	Q94pt4 tamias sibi
698	73.5	6.0	720	2	BAC85085	Bac85085 physcomit	771	73	6.0	379	2	Q94Y74	Q94y74 tamias amoe
699	73.5	6.0	756	2	Q44417	Q44417 chironomus	772	73	6.0	379	2	AA063457	AAo63457 cavia por
700	73.5	6.0	756	2	Q44418	Q86az6 dictyosteli	773	73	6.0	379	2	AA063459	AAo63459 cavia por
701	73.5	6.0	815	2	Q86AZ6	Q62786 rattus norv	774	73	6.0	379	2	AAp73012	AAp73012 genetia j
702	73.5	6.0	879	1	FPRP_RAT	Q86a16 dictyosteli	775	73	6.0	379	2	AAQ08019	AAq08019 civettict
703	73.5	6.0	970	2	Q86AL6	Q88pe4 pseudomonas	776	73	6.0	379	2	AAQ08027	AAq08027 genetia j
704	73.5	6.0	1014	2	Q88PE4	Q92sh0 rhizobium m	777	73	6.0	379	2	CAD87987	Cad87987 platanist
705	73.5	6.0	1061	2	Q92SH0	Q92sh0 rhizobium m	778	73	6.0	380	2	Q7YE29	Q7ye29 neopomacent
706	73.5	6.0	1253	2	Q6CUJ1	Q6cu11 kluveromyc	779	73	6.0	380	2	Q7YHT9	Q7yht9 goodea grac
707	73.5	6.0	1501	2	Q75US9	Q75j89 dictyosteli	780	73	6.0	380	2	Q9T5N4	Q9t5r4 saiga tatar
708	73.5	6.0	1501	2	AA545345	AA545345 dictyoste	781	73	6.0	412	1	AATC_MOUSE	P052C01 mus musculu
709	73.5	6.0	1543	1	MRP2_MOUSE	Q8vi47 mus musculu	782	73	6.0	424	2	Q7P4Z0	Q7p4z0 fusobacteri
710	73.5	6.0	1543	2	Q8VI46	Q8vi46 mus musculu	783	73	6.0	440	2	Q8RCF9	Q8rcp9 thermoanaer
711	73.5	6.0	1605	2	Q8AYF1	Q8ayf1 xenopus lae	784	73	6.0	457	2	Q7RJ14	Q7rj14 plasmodium
712	73.5	6.0	1761	2	Q6CTB0	Q6ctb0 kluveromyc	785	73	6.0	458	1	TCR_BACST	P075611 bacillus st
713	73	6.0	140	2	Q85PI8	Q85pi8 ovis aries	786	73	6.0	458	1	TCR_STRAG	P13924 streptococc
714	73	6.0	196	2	Q7VRH4	Q7vrh4 candidatus	787	73	6.0	458	1	TCR_STRPN	P11063 streptococc
715	73	6.0	215	2	Q6HE74	Q6he74 bacillus th	788	73	6.0	458	2	Q7B6N8	Q7b6n8 enterococcu
716	73	6.0	215	2	Q731K5	Q731k5 bacillus ce	789	73	6.0	458	2	Q79C13	Q79c13 plasmid pbc
717	73	6.0	215	2	Q818Z4	Q818z4 bacillus ce	790	73	6.0	458	2	BAA21837	Baa21837 enterococ
718	73	6.0	215	2	Q81MD5	Q81md5 bacillus an	791	73	6.0	458	2	AAA84918	AAa84918 plasmid p
719	73	6.0	215	2	AA543062	AA543062 bacillus	792	73	6.0	458	2	AAAN03826	AAa03826 enterococ
720	73	6.0	215	2	AAT33434	Aat33434 bacillus	793	73	6.0	458	2	AAAN05731	AAa05731 bacillus
721	73	6.0	256	1	YCA5_YEAST	P25587 saccharomyc	794	73	6.0	458	2	AAB09024	Aab09024 enterococ
722	73	6.0	280	2	Q9K8S9	Q9k8s9 bacillus ha	795	73	6.0	484	2	Q7MB44	Q7mb44 photorhabdu
723	73	6.0	289	1	OPSD_ABYKO	Q42294 abysococcu	796	73	6.0	484	2	Q92PUB	Q92pu8 rhizobium m
724	73	6.0	298	2	Q9A571	Q9a571 caulobacter	797	73	6.0	498	2	Q8ZQ35	Q8zq35 salmonella
725	73	6.0	300	2	Q20849	Q20849 dipsosaurus	798	73	6.0	501	2	Q6GBA3	Q6gba3 staphylococ
726	73	6.0	308	2	Q9PW10	Q9pw10 gallus gall	799	73	6.0	501	2	Q99VP6	Q99vp6 staphylococ
727	73	6.0	312	2	Q8VFE2	Q8vfe2 mus musculu	800	73	6.0	501	2	Q7A1I0	Q7a1i0 staphylococ
728	73	6.0	312	2	AAQ77020	Aaq77020 mus muscu	801	73	6.0	501	2	Q7A6T5	Q7a6t5 staphylococ
729	73	6.0	340	2	Q8HD58	Q8hd58 kannabateom	802	73	6.0	515	2	Q7YS37	Q7ys37 bos indicus
730	73	6.0	352	2	Q93887	Q93887 cryptococcu	803	73	6.0	544	2	Q8UQ37	Q8uj37 avian infec
731	73	6.0	352	2	Q6DY59	Q6dy59 pseudopleur	804	73	6.0	582	2	Q65670	Q65670 arabidopsis
732	73	6.0	354	2	Q6LJK9	Q6ljk9 photobacter	805	73	6.0	679	2	Q9LJY0	Q9ljy0 arabidopsis
733	73	6.0	354	2	CAG22521	Cag22521 photobact	806	73	6.0	707	1	CNAL_HUMAN	Q9ljy0 arabidopsis
734	73	6.0	360	2	Q8HD59	Q8hd59 kannabateom	807	73	6.0	718	1	SL53_CANFA	Q9nx78 homo sapien
735	73	6.0	360	2	Q8HIC1	Q8hici calloscluru	808	73	6.0	852	2	Q8UTB2	P31637 canis famil
736	73	6.0	371	2	Q94Y45	Q94y45 tamias sono	809	73	6.0	870	2	Q6E7I0	Q6e7i0 human immun
737	73	6.0	372	2	Q94Y75	Q94y75 tamias amoe	810	73	6.0	878	2	Q8C6Q7	Q8c6q7 mus musculu
738	73	6.0	373	2	Q94Y48	Q94y48 tamias sene	811	73	6.0	1152	1	CD45_MOUSE	P06800 mus musculu
739	73	6.0	376	2	Q94Y73	Q94y73 tamias amoe	812	73	6.0	1154	2	Q7XPM1	Q7xpm1 oryza sativ
740	73	6.0	379	1	CYB_CERPM	Q9b5r2 cephalophus	813	73	6.0	1224	1	WD11_HUMAN	Q9bzh6 homo sapien
741	73	6.0	379	1	CYB_CEPMO	Q9b5r3 cephalophus	814	73	6.0	1243	2	Q9P2U6	Q9p2j6 homo sapien
742	73	6.0	379	1	CYB_ERIEU	Q36368 erinaceus e	815	73	6.0	1291	2	Q61812	Q618i2 mus musculu
743	73	6.0	379	1	CYB_SHEEP	P24959 ovis aries	816	73	6.0	1343	2	Q64730	Q647j0 mus musculu
744	73	6.0	379	1	CYB_SPEAT	Q9tf14 spermophilu	817	72.5	6.0	117	2	Q6UKG2	Q6ukg2 phoronis ps
745	73	6.0	379	1	CYB_SPEAN	Q9tf89 spermophilu	818	72.5	6.0	117	2	AAR13388	Aar13388 phoronis
746	73	6.0	379	1	CYB_SPEBE	Q9tf89 spermophilu	819	72.5	6.0	144	2	Q95ID9	Q95id9 panteleliella
747	73	6.0	379	1	CYB_SPEBE	Q94y47 tamias sene	820	72.5	6.0	146	2	Q8LU08	Q8luu8 martes amer
748	73	6.0	379	1	CYB_TAMSE	Q20549 ctenomys ha	821	72.5	6.0	146	2	Q8LU09	Q8luu9 martes amer
749	73	6.0	379	2	Q6XAG4	Q6xag4 cavia porce	822	72.5	6.0	215	1	Y457_ANASP	P297J13 anabaena sp
750	73	6.0	379	2	Q6XBW5	Q6xbw5 genetia joh	823	72.5	6.0	254	2	Q8XU90	Q8xu90 enterococcu
751	73	6.0	379	2	Q70RT7	Q70rt7 plataniesta	824	72.5	6.0	275	2	Q6GBU3	Q6gbu3 staphylococ
752	73	6.0	379	2	Q71FU2	Q71fj2 civettictis	825	72.5	6.0	275	2	Q99VF4	Q99vf4 staphylococ
753	73	6.0	379	2	Q8HQF0	Q8hqf0 plecotus au	826	72.5	6.0	275	2	Q7A1D7	Q7a1d7 staphylococ
754	73	6.0	379	2	Q9TDO9	Q9tdq9 muntiacus m	827	72.5	6.0	283	2	Q7A6L0	Q7a6l0 staphylococ
755	73	6.0	379	2	Q9TEF9	Q9tef9 cavia porce	828	72.5	6.0	283	2	Q6G5H9	Q6g5h9 bartonella
756	73	6.0	379	2	Q9TF08	Q9tf08 spermophilu	829	72.5	6.0	288	2	Q6G0Y0	Q6g0y0 bartonella
757	73	6.0	379	2	Q9TF13	Q9tf13 spermophilu	830	72.5	6.0	290	1	YC38_CYAPA	P48278 cyanophora
758	73	6.0	379	2	Q9TF72	Q9tf72 spermophilu	831	72.5	6.0	297	2	Q9A1Y4	Q9a1y4 carsonella
759	73	6.0	379	2	Q9TF87	Q9tf87 spermophilu	832	72.5	6.0	306	2	Q8FKX8	Q8fkx8 escherichia
760	73	6.0	379	2	Q9TGH3	Q9tgh3 tragelaphus	833	72.5	6.0	320	2	Q8NH95	Q8nh35 homo sapien
761	73	6.0	379	2	Q9XLE3	Q9xle3 cephalophus	834	72.5	6.0	343	2	Q85C21	Q85c21 uma paraphy

835	72.5	6.0	379	2	020615	020615 cryptomye h	908	72	5.9	379	2	CAD88013	Cad88013 pontopori
836	72.5	6.0	379	2	06T8R2	06t8r2 spermophilu	909	72	5.9	380	2	003399	003399 acomys sp.
837	72.5	6.0	379	2	07YD73	07yd73 hypsugo sav	910	72	5.9	380	2	07YE28	07ye28 neopomacent
838	72.5	6.0	379	2	09TF06	09tf06 spermophilu	911	72	5.9	380	2	07YHG1	07yhg1 xenotoca va
839	72.5	6.0	379	2	09TF22	09tf22 spermophilu	912	72	5.9	380	2	07YHU0	07yhj0 goodea grac
840	72.5	6.0	379	2	AAR88277	Aar88277 spermophi	913	72	5.9	385	2	06MSW4	06msw4 mycoplasma
841	72.5	6.0	397	2	041536	041536 triticum ae	914	72	5.9	385	2	CAE77274	Caet77274 mycoplaam
842	72.5	6.0	416	2	024725	024725 nocardioid	915	72	5.9	415	2	AAQ18754	Aaql8754 pseudendo
843	72.5	6.0	453	2	084WQ0	084wq0 arabidopsis	916	72	5.9	415	2	AAQ18754	Aaql8754 pseudendo
844	72.5	6.0	509	2	08L4K5	08l4k5 oryza sativ	917	72	5.9	417	2	07YH69	07yh69 taenia asia
845	72.5	6.0	575	2	062657	062657 rattus norv	918	72	5.9	422	2	0736J7	0736j7 bacillus ce
846	72.5	6.0	578	2	0979U5	0979u5 thermoplaam	919	72	5.9	422	2	AAS41815	Aas41815 bacillus
847	72.5	6.0	586	2	08S279	08s279 oryza sativ	920	72	5.9	441	1	YCDQ_ECOLI	P75905 escherichia
848	72.5	6.0	606	2	09XXR3	09xxr3 caenorhabdi	921	72	5.9	441	2	07AFM3	07afm3 escherichia
849	72.5	6.0	616	1	56AK_RAT	064093 rattus norv	922	72	5.9	441	2	08FJ31	08fj31 escherichia
850	72.5	6.0	619	2	062701	062701 rattus norv	923	72	5.9	441	2	08XAR5	08xar5 escherichia
851	72.5	6.0	623	2	07S238	07s238 neurospora	924	72	5.9	443	2	07V6J9	07v6j9 prochloroco
852	72.5	6.0	623	2	07MCW8	07mcw8 vibrio vuln	925	72	5.9	447	2	092YLS	092y15 rhizobium m
853	72.5	6.0	640	2	088A50	088a50 pseudomonas	926	72	5.9	449	2	06L279	06l279 picrophilus
854	72.5	6.0	660	2	07V3L0	07v3l0 prochloroco	927	72	5.9	455	2	045936	045936 caenorhabdi
855	72.5	6.0	794	2	07R595	07r595 giardia lam	928	72	5.9	458	2	08RLD5	08rlid5 enterococcu
856	72.5	6.0	904	2	059666	059666 schizosacch	929	72	5.9	459	2	094Q77	094q77 mirza coque
857	72.5	6.0	1032	2	09CL57	09cl57 pasteurella	930	72	5.9	459	2	094YD5	094yd5 sorex ungui
858	72.5	6.0	1073	2	09WIT8	09wit8 drosophila	931	72	5.9	475	2	074315	074315 schizosacch
859	72.5	6.0	1243	2	093564	093564 caenorhabdi	932	72	5.9	483	2	09G8V8	09g8v8 rhodomonas
860	72.5	6.0	1467	2	07RHL5	07rhl5 plasmodium	933	72	5.9	534	2	06Y411	06y411 ophiura lut
861	72	5.9	128	2	003245	003245 opius dissi	934	72	5.9	534	2	AAO65628	Aao65628 ophiura 1
862	72	5.9	128	2	P92861	P92861 pauesia jun	935	72	5.9	579	2	057322	057322 ambystoma t
863	72	5.9	142	2	08HIRI	08hir1 braunsapis	936	72	5.9	581	1	PRLR_CEREL	Q28235 cervus elap
864	72	5.9	144	2	08L8T4	08l8t4 arabidopsis	937	72	5.9	607	2	08LPM4	Q28235 cervus elap
865	72	5.9	220	2	06RBY2	06rby2 marmota mon	938	72	5.9	617	2	09VE46	08lpm4 citrus sine
866	72	5.9	220	2	AAR90236	Aar90236 marmota m	939	72	5.9	614	2	06S272	09ve46 drosophila
867	72	5.9	253	2	08AWK7	08awk7 trachinus d	940	72	5.9	786	2	09XF71	06s272 arabidopsis
868	72	5.9	253	2	08AMN9	08amn9 forsterygio	941	72	5.9	854	2	093244	09xf71 nicotiana t
869	72	5.9	262	2	07Y650	07y650 plataniasta	942	72	5.9	904	2	06NB24	093244 oncorhynchu
870	72	5.9	289	1	0PSD_BATMU	042300 batrachocot	943	72	5.9	904	2	CAE26126	06nb24 rhodopseuo
871	72	5.9	301	2	08JMA5	08jma5 mamestra co	944	72	5.9	913	2	06BIQ9	Caet26126 rhodopseu
872	72	5.9	309	2	09V4C6	09vac6 drosophila	945	72	5.9	916	2	09VT80	06biq9 debaryomyce
873	72	5.9	309	2	AAF59351	Aaf59351 drosophil	946	72	5.9	982	1	YS96_CAEEL	09vt80 drosophila
874	72	5.9	328	2	08UV77	08uv77 brachydanio	947	72	5.9	1022	2	083DH8	09965 caenorhabdi
875	72	5.9	330	2	085T13	085t13 anolis roqu	948	72	5.9	1079	2	0703G5	Q83dh8 coxiella bu
876	72	5.9	330	2	085T23	085t23 anolis roqu	949	72	5.9	1079	2	CAF22245	0703g5 ustilago ma
877	72	5.9	330	2	085T28	085t28 anolis roqu	950	72	5.9	1178	2	09NF95	Caet22245 ustilago
878	72	5.9	344	2	08YQ35	08yq35 anabaena sp	951	72	5.9	1253	2	Q19523	Q19f95 leishmania
879	72	5.9	375	2	06LYB9	06lyb9 methanococc	952	72	5.9	1444	2	095XW0	Q19523 caenorhabdi
880	72	5.9	375	2	CAF30628	Caef30628 methanoco	953	72	5.9	1449	2	08T675	086f75 dictyosteli
881	72	5.9	378	2	094Y42	094y42 tamias stri	954	72	5.9	1583	1	MISA_SCHPO	009725 schizosacch
882	72	5.9	378	2	072H63	072h63 thermus the	955	72	5.9	118	2	0864T7	0864t7 ornithorhyn
883	72	5.9	378	2	AAS81974	Aas81974 thermus t	956	71.5	5.9	128	2	079128	079128 braunsiapis
884	72	5.9	379	1	CYB_GAZGA	048336 gazella gaz	957	71.5	5.9	142	2	08HIQ9	08hiq9 brevineura
885	72	5.9	379	1	CYB_LUTLU	034900 lutra lutra	958	71.5	5.9	146	2	08LXB9	08lxb9 martes amer
886	72	5.9	379	1	CYB_MARFA	09tcb4 martes flav	959	71.5	5.9	146	2	08LXC0	Q8lxc0 martes amer
887	72	5.9	379	1	CYB_MARFL	09xmcl marmota fla	960	71.5	5.9	152	2	06MZ91	Q6mz91 mycobacteri
888	72	5.9	379	1	CYB_MARZI	09tcb5 martes zibe	961	71.5	5.9	152	2	CAE46824	Caet46824 mycobacte
889	72	5.9	379	1	CYB_ORYLE	09tcb8 martes zibe	962	71.5	5.9	183	2	09VHG9	Q9vhg9 drosophila
890	72	5.9	379	2	06XAG1	06xag1 cavia teschu	963	71.5	5.9	202	2	06ZV02	06zv02 homo sapien
891	72	5.9	379	2	06XBM7	06xbw7 viverricula	964	71.5	5.9	202	2	BAC86064	Bac86064 homo sapi
892	72	5.9	379	2	070RRI	070rr1 pontoporia	965	71.5	5.9	235	2	06DR08	06dr08 arabidopsis
893	72	5.9	379	2	071FI1	071fi1 genetia gen	966	71.5	5.9	235	2	06E283	Q6et283 arabidopsis
894	72	5.9	379	2	07YBY4	07yby4 myotis tric	967	71.5	5.9	268	2	06XFA2	Q6xfa2 malpion mo
895	72	5.9	379	2	033949	033949 bubalus bub	968	71.5	5.9	268	2	AAP78954	Aap78954 malpion
896	72	5.9	379	2	036096	036096 trinomys pa	969	71.5	5.9	299	2	06BQG8	Q6bqg8 debaryomyce
897	72	5.9	379	2	085PM8	085pm8 paradoxurus	970	71.5	5.9	307	2	07RP65	Q7rp65 plasmodium
898	72	5.9	379	2	09T4L9	09t4l9 martes zibe	971	71.5	5.9	314	2	08VPZ5	Q8vpz5 mus musculu
899	72	5.9	379	2	09TEB6	09teb6 martes zibe	972	71.5	5.9	332	2	093ZH9	Q93zh9 arabidopsis
900	72	5.9	379	2	09TF86	09tf86 spermophilu	973	71.5	5.9	343	2	085AL2	Q85al2 uma scopari
901	72	5.9	379	2	09MNV1	09mnv1 martes mart	974	71.5	5.9	343	2	085AT3	Q8sat3 uma scopari
902	72	5.9	379	2	09MNV3	09mnv3 martes amer	975	71.5	5.9	343	2	085KN7	Q8skn7 uma paraphy
903	72	5.9	379	2	094Y41	094y41 tamias stri	976	71.5	5.9	343	2	085KP3	Q85kp3 uma exaul.
904	72	5.9	379	2	08W8Q1	08w8q1 martes foin	977	71.5	5.9	343	2	09B4H4	Q9b4h4 uma scopari
905	72	5.9	379	2	AAO63462	Aao63462 cavia tbc	978	71.5	5.9	343	2	Q9B4H6	Q9b4h6 uma scopari
906	72	5.9	379	2	AAP73010	Aap73010 viverricu	979	71.5	5.9	349	2	Q899J8	Q899j8 clostridium
907	72	5.9	379	2	AAQ08030	Aaq08030 genetia g	980	71.5	5.9	353	2	Q7Z1Q4	Q7z1q4 caenorhabdi

981	71.5	5.9	353	2	Q9F0B7	Q9f0b7 lactobacill	1054	71	5.8	288	2	Q82TA5	O82ta5 nitrosomona
982	71.5	5.9	354	1	OPSD_ZEUPA	O42604 zeus faber	1055	71	5.8	289	1	OPSD_PROJE	O42451 procottus j
983	71.5	5.9	356	2	Q9GCR8	Q9gcr8 belomys pea	1056	71	5.8	299	1	T2R3_RAT	O9jku0 rattus norv
984	71.5	5.9	363	1	MRAY_TREDA	O83365 treponema p	1057	71	5.8	312	2	Q8Q0I2	O8q012 methanosarc
985	71.5	5.9	366	1	YB96_METUA	O58596 methanococc	1058	71	5.8	329	2	Q71FI5	O71fi5 osbornictis
986	71.5	5.9	378	2	O94X35	O94x35 cymatogaste	1059	71	5.8	329	2	AAQ08026	AaQ08026 osbornict
987	71.5	5.9	379	1	CYB_LAMPA	O34916 lama guanac	1060	71	5.8	330	2	O85T24	O85t24 anolis roqu
988	71.5	5.9	379	2	O6T8R5	O6t8r5 spermophilu	1061	71	5.8	330	2	O85T27	O85t27 anolis roqu
989	71.5	5.9	379	2	O6T8R6	O6t8r6 spermophilu	1062	71	5.8	344	1	YK58_ARCFU	O28221 archaeglob
990	71.5	5.9	379	2	O7YE02	O7ye02 stegastes p	1063	71	5.8	345	1	O98PL6	O98pl6 mycoplasma
991	71.5	5.9	379	2	Q9TF62	Q9tf62 spermophilu	1064	71	5.8	356	2	IGT_MYCPE	O8ewa4 mycoplasma
992	71.5	5.9	379	2	O9TF68	Q9tf68 spermophilu	1065	71	5.8	356	2	Q9GCR2	O9gcr2 petaurista
993	71.5	5.9	379	2	Q94WM6	Q94w6 ctenomys la	1066	71	5.8	356	2	O9GCR9	O9gcr9 glaucomys v
994	71.5	5.9	379	2	Q94WM7	O94w7 ctenomys la	1067	71	5.8	360	2	O85Q50	O85q50 thrichomys
995	71.5	5.9	379	2	AAAR88273	AaAR88273 spermophi	1068	71	5.8	360	2	O72S76	O72s76 leptospira
996	71.5	5.9	379	2	AAAR88274	AaAR88274 spermophi	1069	71	5.8	360	2	O8E3G4	O8f3c4 leptospira
997	71.5	5.9	381	1	CYB_SMIMA	O20433 smintropsis	1070	71	5.8	360	2	AA570106	Aa570106 leptospir
998	71.5	5.9	381	2	Q9XP74	Q9xp74 smintropsis	1071	71	5.8	365	2	O85Q59	O85q59 thrichomys
999	71.5	5.9	386	2	Q8ZFC4	O8zfc4 yersinia pe	1072	71	5.8	370	2	O85Q45	O85q45 thrichomys
1000	71.5	5.9	386	2	AA561835	Aa561835 yersinia	1073	71	5.8	370	2	O85Q51	O85q51 thrichomys
1001	71.5	5.9	398	1	TRFR_HUMAN	P34981 homo sapien	1074	71	5.8	374	2	O85Q47	O85q47 thrichomys
1002	71.5	5.9	398	2	AAAR84356	AaAR84356 homo sapi	1075	71	5.8	375	2	O91NH5	O91nh5 arabidopsis
1003	71.5	5.9	424	2	Q7VMU9	Q7vmu9 haemophilus	1076	71	5.8	377	2	Q94Y54	O94y54 tamias ochr
1004	71.5	5.9	429	2	O6GIZ4	O6giz4 staphylococ	1077	71	5.8	378	2	Q71FH4	O71fh4 mungotictis
1005	71.5	5.9	444	2	O34502	O34502 bacillus su	1078	71	5.8	378	2	AAQ08037	AaQ08037 mungotict
1006	71.5	5.9	445	2	O8CNG8	O8cng8 staphylococ	1079	71	5.8	379	1	CYB_BUBBU	O33950 bubalus bub
1007	71.5	5.9	449	2	Q7W0C7	O63853 sarcophyton	1080	71	5.8	379	1	CYB_CEBPM	O93dl2 cephalorhyn
1008	71.5	5.9	495	2	O63853	O63853 sarcophyton	1081	71	5.8	379	1	CYB_CEBEU	O9tdl3 cephalorhyn
1009	71.5	5.9	509	2	Q8L481	O8l481 oryza sativ	1082	71	5.8	379	1	CYB_CEBHA	O9tdl5 cephalorhyn
1010	71.5	5.9	527	2	Q9FMH4	O9fmh4 arabidopsis	1083	71	5.8	379	1	CYB_GIAVO	O9tfi3 glaucomys v
1011	71.5	5.9	540	2	Q98Y24	O98y24 avian infec	1084	71	5.8	379	1	CYB_MYOEM	O957h3 myotis emar
1012	71.5	5.9	542	2	O8S016	O8s016 oryza sativ	1085	71	5.8	379	1	CYB_PONBL	O9mg84 pontoporia
1013	71.5	5.9	581	1	FRIZ_DROME	P18537 drosophila	1086	71	5.8	379	2	O20539	O20539 ctenomys le
1014	71.5	5.9	600	2	O77387	O77387 plasmodium	1087	71	5.8	379	2	O20544	O20544 ctenomys le
1015	71.5	5.9	616	2	Q7PX39	Q7px39 anopheles g	1088	71	5.8	379	2	O20968	O20968 tregelaphus
1016	71.5	5.9	677	2	Q7YKV9	Q7ykv9 rhynchospor	1089	71	5.8	379	2	O099340	O099340 oreotragus
1017	71.5	5.9	743	2	Q9GEZ4	Q9gez4 gilia rigid	1090	71	5.8	379	2	O099343	O099343 tregelaphus
1018	71.5	5.9	784	2	Q9CIF4	O9cif4 lactococcus	1091	71	5.8	379	2	P92568	P92568 bubalus bub
1019	71.5	5.9	860	2	Q71AY5	Q71ay5 human immu	1092	71	5.8	379	2	P92570	P92570 bubalus bub
1020	71.5	5.9	860	2	AAQ10908	AaQ10908 human imm	1093	71	5.8	379	2	P92890	P92890 bubalus bub
1021	71.5	5.9	863	2	Q73355	Q73355 human immu	1094	71	5.8	379	2	P92899	P92899 bubalus bub
1022	71.5	5.9	863	2	Q73356	Q73356 human immu	1095	71	5.8	379	2	Q6X9U4	Q6x9u4 cavia porce
1023	71.5	5.9	880	2	O8Y8Q5	O8y8q5 listeria mo	1096	71	5.8	379	2	Q6XBT5	O6xbt5 genetia gen
1024	71.5	5.9	880	2	Q721X6	Q721x6 listeria mo	1097	71	5.8	379	2	Q6XBM6	Q6xbm6 poiana rich
1025	71.5	5.9	880	2	AAAT03638	AaAT03638 listeria	1098	71	5.8	379	2	O6XKD9	O6xkd9 cavia porce
1026	71.5	5.9	968	2	Q6ZU25	Q6zu25 homo sapien	1099	71	5.8	379	2	Q71FH9	O71fh9 paradoxurus
1027	71.5	5.9	968	2	BAC86402	Bac86402 homo sapi	1100	71	5.8	379	2	Q71BW1	O71bw1 glaucomys s
1028	71.5	5.9	1029	2	Q9F8V7	Q9f8v7 agrobacteri	1101	71	5.8	379	2	O7YD72	O7ydl2 myotis goud
1029	71.5	5.9	1029	2	O8UCES	O8uces agrobacteri	1102	71	5.8	379	2	Q34661	Q34661 glaucomys s
1030	71.5	5.9	1029	2	O8UCES	O8uces agrobacteri	1103	71	5.8	379	2	O85PN8	O85pn8 galidictis
1031	71.5	5.9	1043	2	O8ZCE8	O8zce8 yersinia pe	1104	71	5.8	379	2	Q85Q58	Q85q58 thrichomys
1032	71.5	5.9	1085	2	Q74SE6	Q74se6 yersinia pe	1105	71	5.8	379	2	Q8HBS5	O8hb35 camelus dro
1033	71.5	5.9	1085	2	AA562858	Aa562858 yersinia	1106	71	5.8	379	2	Q8HDS6	O8hd36 myocastor c
1034	71.5	5.9	1148	1	A8A2_HUMAN	O9nti2 homo sapien	1107	71	5.8	379	2	Q8LZE1	O8lzel civettictis
1035	71.5	5.9	1188	2	O6ZSP3	O6zsp3 homo sapien	1108	71	5.8	379	2	Q9TFI1	O9tfi1 spermophilu
1036	71.5	5.9	1188	2	BAC86905	Bac86905 homo sapi	1109	71	5.8	379	2	Q9TFI2	O9tfi2 spermophilu
1037	71.5	5.9	1424	2	Q9VLA2	Q9vla2 drosophila	1110	71	5.8	379	2	Q9TGH6	O9tgh6 antilope ce
1038	71.5	5.9	1543	2	Q9JIH8	Q9jih8 mus musculu	1111	71	5.8	379	2	Q9XLD5	O9xld5 kobus leche
1039	71.5	5.9	1662	2	Q8T6J2	Q8t6j2 dictyostell	1112	71	5.8	379	2	Q9XLD6	O9xld6 kobus leche
1040	71.5	5.9	1805	2	Q7QVW0	Q7qvwo giardia lam	1113	71	5.8	379	2	Q9XLD7	O9xld7 kobus leche
1041	71.5	5.8	135	2	Q6V9B7	Q6v9b7 penicillium	1114	71	5.8	379	2	Q9MLD7	Q9mlj3 mustela alt
1042	71	5.8	135	2	AAQ54933	AaQ54933 penicilli	1115	71	5.8	379	2	Q9B5R5	Q9b5r5 cephalophus
1043	71	5.8	193	2	O6PI73	O6pi73 homo sapien	1116	71	5.8	379	2	Q9G3S4	Q9g334 pteropus sc
1044	71	5.8	193	2	AAH41708	AaH41708 homo sapi	1117	71	5.8	379	2	Q9G7T9	Q9g7c9 platanieta
1045	71	5.8	216	1	SSPN_MOUSE	O62147 mus musculu	1118	71	5.8	379	2	Q9GBG9	Q9gbg9 pontoporia
1046	71	5.8	233	2	Q9VCF1	Q9vcf1 drosophila	1119	71	5.8	379	2	Q9GBH1	Q9gbh1 martes foin
1047	71	5.8	244	2	O81JU6	O81ju6 bacillus an	1120	71	5.8	379	2	Q952R3	Q952r3 glaucomys s
1048	71	5.8	244	2	AAAT34745	AaAT34745 bacillus	1121	71	5.8	379	2	AAO63463	AaO63463 myotis muri
1049	71	5.8	247	2	O6CNU9	O6cni9 kluveromyc	1122	71	5.8	379	2	AAO43119	AaO43119 cavia por
1050	71	5.8	253	2	Q8AMK6	O8awk6 uranoscopus	1123	71	5.8	379	2	AAO43121	AaO43121 cavia por
1051	71	5.8	254	2	Q9CNU5	Q9cnu5 pasteurella	1124	71	5.8	379	2		
1052	71	5.8	262	2	Q7YJ76	Q7yj76 platanieta	1125	71	5.8	379	2		
1053	71	5.8	263	2	Q7J6C3	Q7j6c3 glaucomys s	1126	71	5.8	379	2		

1127	71	5.8	379	2	AAP73011	Aap73011 poiana ri	1200	70.5	5.8	289	2	Q80IF6	Q80if6 human herpe
1128	71	5.8	379	2	AAP73042	Aap73042 geneteta g	1201	70.5	5.8	293	2	Q8V911	Q8v911 squash ye11
1129	71	5.8	379	2	AAQ08032	Aaq08032 paradoxur	1202	70.5	5.8	297	2	Q88HV6	Q88hv6 pseudomonas
1130	71	5.8	380	2	Q9TIX5	Q9tcx5 capra hircu	1203	70.5	5.8	309	2	Q8VER8	Q8ver8 mus musculu
1131	71	5.8	380	2	Q9T7N0	Q9t7n0 cricetomys	1204	70.5	5.8	314	2	Q7TRU3	Q7tru3 mus musculu
1132	71	5.8	388	2	Q8D344	Q8d344 wigglewort	1205	70.5	5.8	315	1	QAA4 HUMAN	Q8em89 oceanobacil
1133	71	5.8	411	2	Q7V8Z6	Q7v8z6 prochloroco	1206	70.5	5.8	317	2	Q8EM89	Q8em89 oceanobacil
1134	71	5.8	421	2	Q8GMJ7	Q8gmj7 escherichia	1207	70.5	5.8	324	2	Q6IFR1	Q6iffr1 homo sapien
1135	71	5.8	429	1	ARSB STAM	Q9rc95 staphylococ	1208	70.5	5.8	343	2	Q85KN4	Q85kn4 uma scopari
1136	71	5.8	430	2	Q6Y0M1	Q6y0m1 staphylococ	1209	70.5	5.8	343	2	Q9B4H1	Q9b4h1 holbrookia
1137	71	5.8	430	2	Q6Y0N3	Q6y0n3 staphylococ	1210	70.5	5.8	347	2	Q6YIU7	Q6yiu7 uta stansbu
1138	71	5.8	430	2	Q8GON2	Q8ggn2 staphylococ	1211	70.5	5.8	347	2	Q9MM75	Q9mm75 psammodromu
1139	71	5.8	430	2	AAP32336	Aap32336 staphyloc	1212	70.5	5.8	347	2	AAO65536	Aao65536 uta stans
1140	71	5.8	430	2	AAP32340	Aap32340 staphyloc	1213	70.5	5.8	349	2	Q8STH4	Q8sth4 melipona bi
1141	71	5.8	430	2	AAP32348	Aap32348 staphyloc	1214	70.5	5.8	352	1	OPSD_ASTFA	P41590 astyanax fa
1142	71	5.8	448	2	Q6CHS9	Q6chs9 yarrowia li	1215	70.5	5.8	356	2	Q9G0Y5	Q9g0y5 petaurista
1143	71	5.8	448	2	Q863Y8	Q863y8 papio hamad	1216	70.5	5.8	369	2	Q89UJ1	Q89uj1 bradyrhizob
1144	71	5.8	466	2	Q8DL03	Q8dl03 synecococc	1217	70.5	5.8	370	2	Q87M50	Q87m50 vibrio para
1145	71	5.8	471	2	Q85YM2	Q85ym2 euphorbia g	1218	70.5	5.8	374	1	PILC_PSEAE	P22609 pseudomonas
1146	71	5.8	471	2	Q6LSU9	Q6lsu9 photobacter	1219	70.5	5.8	379	1	CYB_CYNLE	Q9tf51 spermophilu
1147	71	5.8	471	2	CAG19627	Cag19627 photobact	1220	70.5	5.8	379	1	CYB_MARBA	Q9tf51 spermophilu
1148	71	5.8	473	2	Q887D3	Q887d3 pseudomonas	1221	70.5	5.8	379	1	CYB_SPEAR	Q9tf57 spermophilu
1149	71	5.8	474	1	LCTP_STRIN	Q33654 streptococc	1222	70.5	5.8	379	1	CYB_SPEAR	Q9tf57 spermophilu
1150	71	5.8	487	2	Q9YG70	Q9yg70 aeropyrum p	1223	70.5	5.8	379	1	CYB_SPEAR	Q9tf57 spermophilu
1151	71	5.8	504	2	Q9TBZ6	Q9tbz6 lampromia a	1224	70.5	5.8	379	1	CYB_SPEAR	Q9tf57 spermophilu
1152	71	5.8	518	2	Q7MR21	Q7mr21 wolinnella s	1225	70.5	5.8	379	2	Q6T8P2	Q6t8p2 spermophilu
1153	71	5.8	527	2	Q8BYW9	Q8byw9 mus musculu	1226	70.5	5.8	379	2	Q6XBV0	Q6xbv0 geneteta gen
1154	71	5.8	551	1	HGT1_KLULA	P49374 kluyveromyc	1227	70.5	5.8	379	2	Q7Y6P3	Q7y6p3 lagenorhync
1155	71	5.8	551	2	Q7U9K1	Q7u9k1 synecococc	1228	70.5	5.8	379	2	Q7Y8S1	Q7y8s1 lagenorhync
1156	71	5.8	556	2	Q9FFK3	Q9ffk3 arabidopsis	1229	70.5	5.8	379	2	Q7Y8E1	Q7y8e1 lagenorhync
1157	71	5.8	574	2	Q17902	Q17902 caenorhabdi	1230	70.5	5.8	379	2	Q7YDE8	Q7yde8 lagenorhync
1158	71	5.8	622	2	Q95Y58	Q95y58 caenorhabdi	1231	70.5	5.8	379	2	Q7YDE9	Q7yde9 lagenorhync
1159	71	5.8	660	2	Q8LI58	Q8li58 oscillatori	1232	70.5	5.8	379	2	Q7YDF0	Q7ydf0 lagenorhync
1160	71	5.8	712	2	Q8YZ31	Q8yz31 anabaena sp	1233	70.5	5.8	379	2	Q7YDF1	Q7ydf1 lagenorhync
1161	71	5.8	718	1	SL53_BOVIN	P53793 bos taurus	1234	70.5	5.8	379	2	Q7YDF2	Q7ydf2 lagenorhync
1162	71	5.8	815	2	Q7WU49	Q7wu49 bacteroides	1235	70.5	5.8	379	2	Q34235	Q34235 ctenomys so
1163	71	5.8	837	2	Q7TIT7	Q7tlt7 fugu rubrip	1236	70.5	5.8	379	2	Q85PP2	Q85pp2 cryptoproct
1164	71	5.8	852	2	Q6CLB3	Q6clb3 kluyveromyc	1237	70.5	5.8	379	2	Q9TS6	Q9ts6 spermophilu
1165	71	5.8	898	2	Q86JG0	Q86jg0 dictyosteli	1238	70.5	5.8	379	2	Q9T429	Q9t429 spermophilu
1166	71	5.8	1048	2	Q6V6X8	Q6v6x8 pseudomonas	1240	70.5	5.8	379	2	Q9T4W4	Q9t4w4 spermophilu
1168	71	5.8	1048	2	AAQ92181	Aaq92181 pseudomon	1241	70.5	5.8	379	2	Q9TF09	Q9tf09 spermophilu
1169	71	5.8	1059	2	Q6F8F6	Q6f8f6 acinetobact	1242	70.5	5.8	379	2	Q9TF15	Q9tf15 spermophilu
1170	71	5.8	1072	2	Q7UT6	Q7ut6 rhodopirell	1243	70.5	5.8	379	2	Q9TF16	Q9tf16 spermophilu
1171	71	5.8	1246	1	VP03_SHV21	Q01000 salmirine	1244	70.5	5.8	379	2	Q9TF19	Q9tf19 spermophilu
1172	71	5.8	1398	2	Q869T5	Q869t5 dictyosteli	1245	70.5	5.8	379	2	Q9TF23	Q9tf23 spermophilu
1173	71	5.8	1676	2	Q7R124	Q7r124 giardia lam	1246	70.5	5.8	379	2	Q9TF24	Q9tf24 spermophilu
1174	71	5.8	1690	2	Q76P31	Q76p31 dictyosteli	1247	70.5	5.8	379	2	Q9TF25	Q9tf25 spermophilu
1175	71	5.8	1690	2	AAS38615	Aas38615 dictyoste	1248	70.5	5.8	379	2	Q9TF33	Q9tf33 cynomys gun
1176	71	5.8	3094	2	Q6UDW3	Q6udw3 plasmodium	1249	70.5	5.8	379	2	Q9TF40	Q9tf40 spermophilu
1177	71	5.8	3094	2	AAQ73930	Aaq73930 plasmodi	1250	70.5	5.8	379	2	Q9TF63	Q9tf63 spermophilu
1178	71	5.8	92	2	Q8HIR7	Q8hir7 brevineura	1251	70.5	5.8	379	2	Q9TF76	Q9tf76 spermophilu
1179	70.5	5.8	113	2	Q9HDD5	Q9hdd5 flammulina	1252	70.5	5.8	379	2	Q9TF90	Q9tf90 spermophilu
1180	70.5	5.8	140	2	Q9XMB2	Q9xmb2 palorus rat	1253	70.5	5.8	379	2	Q9TF90	Q9tf90 spermophilu
1181	70.5	5.8	141	2	Q99814	Q99814 ixodes hexa	1254	70.5	5.8	379	2	Q9TF99	Q9tf99 spermophilu
1182	70.5	5.8	142	2	Q8HIM4	Q8him4 exoneura an	1255	70.5	5.8	379	2	Q9TH52	Q9th52 marmota men
1183	70.5	5.8	173	2	Q9MGD0	Q9mgd0 penaeus mon	1256	70.5	5.8	379	2	Q9XP32	Q9xp32 marmota men
1184	70.5	5.8	222	2	Q64901	Q64901 arctic grou	1257	70.5	5.8	379	2	Q9B9G0	Q9b9g0 cryptoproct
1185	70.5	5.8	223	1	FXB2_ARATH	Q22870 arabidopsis	1258	70.5	5.8	379	2	Q94WY7	Q94wy7 ctenomys ar
1186	70.5	5.8	223	1	AAM45036	Aam45036 arabidops	1259	70.5	5.8	379	2	AA888296	Aa888296 spermophi
1187	70.5	5.8	229	1	PRL_BOVIN	P01239 bos taurus	1260	70.5	5.8	379	2	AA888297	Aa888297 spermophi
1188	70.5	5.8	230	2	Q97SN8	Q97sn8 streptococc	1261	70.5	5.8	379	2	AA888298	Aa888298 spermophi
1189	70.5	5.8	236	2	Q8DR93	Q8dr93 streptococc	1262	70.5	5.8	379	2	AA888299	Aa888299 spermophi
1190	70.5	5.8	239	2	Q9MIV9	Q9miv9 arabidopsis	1263	70.5	5.8	379	2	AA888300	Aa888300 spermophi
1191	70.5	5.8	243	2	Q8WEL4	Q8wel4 pogonomyrme	1264	70.5	5.8	379	2	AA888301	Aa888301 spermophi
1192	70.5	5.8	245	2	Q84HD8	Q84hd8 vibrio vuln	1265	70.5	5.8	379	2	AA888302	Aa888302 spermophi
1193	70.5	5.8	248	2	Q88NY3	Q88ny3 pseudomonas	1266	70.5	5.8	379	2	AA888303	Aa888303 spermophi
1194	70.5	5.8	266	2	Q34997	Q34997 mesomys his	1267	70.5	5.8	379	2	AA660330	Aa660330 cryptopro
1195	70.5	5.8	274	2	Q995A8	Q995a8 human herpe	1268	70.5	5.8	379	2	AA673027	Aa673027 geneteta g
1196	70.5	5.8	282	1	VMSA_WHYW6	P11293 woodchuck h	1269	70.5	5.8	380	2	Q7YE01	Q7ye01 embiotoca 1
1197	70.5	5.8	282	2	Q64900	Q64900 arctic grou	1270	70.5	5.8	380	2	Q9T7N1	Q9t7n1 cricetomys
1198	70.5	5.8	286	2	Q9P2Y3	Q9p2y3 homo sapien	1271	70.5	5.8	420	2	Q9MIR8	Q9mir8 arabidopsis
1199	70.5	5.8	289	2	Q80IF0	Q80if0 human herpe	1272	70.5	5.8	427	2	Q64899	Q64899 arctic grou



1273	70.5	5.8	433	2	Q92M74	Q92m74 rhizobium m	1346	70	5.8	290	2	CAG23680	Cag23680 photobact
1274	70.5	5.8	446	2	Q92BV5	Q92bv5 streptomyce	1347	70	5.8	300	2	Q33966	Q33966 brachylophu
1275	70.5	5.8	451	2	Q9BHH1	Q9bhh1 leishmania	1348	70	5.8	317	1	ODC3_HUMAN	Q8ngi6 homo sapien
1276	70.5	5.8	454	2	Q9GLZ6	Q9glz6 macaca fasc	1349	70	5.8	330	2	Q85T26	Q85t26 anolis rogu
1277	70.5	5.8	474	2	Q978G5	Q978g5 thermoplas	1350	70	5.8	339	2	Q85HE8	Q85hu8 calliicebus
1278	70.5	5.8	477	2	Q9ABD8	Q9abd8 caulobacter	1351	70	5.8	345	2	Q70GDS	Q70gd5 pasteurella
1279	70.5	5.8	480	2	Q9B970	Q9b970 ceratobolen	1352	70	5.8	345	2	CAE46554	Caee46554 pasteurel
1280	70.5	5.8	482	2	Q9KHJ5	Q9khj5 streptomyce	1353	70	5.8	347	2	Q6IF52	Q6if52 homo sapien
1281	70.5	5.8	490	2	Q8MPG5	Q8mpg5 trypanosoma	1354	70	5.8	353	1	OPSD_MYISO	Q9ygh5 solea solea
1282	70.5	5.8	490	2	Q8MPG7	Q8mpg7 trypanosoma	1355	70	5.8	354	1	OPSD_POERE	P79g48 poecillia re
1283	70.5	5.8	490	2	Q8MPG8	Q8mpg8 trypanosoma	1356	70	5.8	356	2	Q9G236	Q9g236 petaurista
1284	70.5	5.8	504	2	Q95989	Q95989 tegeticula	1357	70	5.8	356	2	Q9GCT0	Q9gct0 petaurista
1285	70.5	5.8	506	2	Q9I1R0	Q9i1r0 pseudomonas	1358	70	5.8	356	2	Q9GCT1	Q9gct1 petaurista
1286	70.5	5.8	518	2	Q6DVG6	Q6dv66 podura aqua	1359	70	5.8	358	2	Q8EMS4	Q8emu4 oceanobacil
1287	70.5	5.8	522	2	Q9K291	Q9k291 chlamydia p	1360	70	5.8	376	2	O20614	O20614 cryptomys h
1288	70.5	5.8	542	2	O55341	O55341 avian infec	1361	70	5.8	376	2	Q94Y43	Q94y43 tamias stri
1289	70.5	5.8	542	2	O55342	O55342 avian infec	1362	70	5.8	379	1	CYB_BOSTR	Q79311 boselaphus
1290	70.5	5.8	544	2	Q917L7	Q917l7 avian infec	1363	70	5.8	379	1	CYB_CYSGR	Q34760 hippotrachus
1291	70.5	5.8	550	2	Q6P0C2	Q6p0c2 brachydanio	1364	70	5.8	379	1	CYB_HIPNI	Q34070 cytelophora
1292	70.5	5.8	550	2	AAH65675	Aah65675 brachydan	1365	70	5.8	379	1	CYB_MARBB	Q9th45 marmota bob
1293	70.5	5.8	561	2	Q917N9	Q917n9 drosophila	1366	70	5.8	379	1	CYB_MYOMO	Q957u4 myotis mont
1294	70.5	5.8	591	2	Q9Z8G2	Q9z8g2 chlamydia p	1367	70	5.8	379	1	CYB_PROCY	Q9g2u7 proechimys
1295	70.5	5.8	591	2	Q9JSF3	Q9jsf3 chlamydia p	1368	70	5.8	379	1	CYB_TRANA	P24965 tragulus na
1296	70.5	5.8	592	2	Q7VQ32	Q7vg32 chlamydia p	1369	70	5.8	379	1	CYB_TURTR	Q9tdj9 turlops tr
1297	70.5	5.8	592	2	Q8VDB9	Q8vdb9 mus musculu	1370	70	5.8	379	2	O79327	Q79337 cephalophus
1298	70.5	5.8	594	2	O80605	O80605 arabidopsis	1371	70	5.8	379	2	O79360	Q79360 kobus megac
1299	70.5	5.8	595	2	Q8L600	Q8l600 arabidopsis	1372	70	5.8	379	2	O99346	O99346 gazella dam
1300	70.5	5.8	595	2	Q9C9Z1	Q9c9z1 arabidopsis	1373	70	5.8	379	2	Q6KFX39	Q6kfx39 saquinus mi
1301	70.5	5.8	619	2	Q758Z0	Q758z0 ashbya goss	1374	70	5.8	379	2	Q6T8N2	Q6t8n2 spermophilu
1302	70.5	5.8	619	2	AA552307	Aa552307 ashbya go	1375	70	5.8	379	2	Q6T8N3	Q6t8n3 spermophilu
1303	70.5	5.8	645	2	Q6GE82	Q6ge82 staphylococ	1376	70	5.8	379	2	Q6T8N4	Q6t8n4 spermophilu
1304	70.5	5.8	685	2	Q8EJ17	Q8ej17 shewanella	1377	70	5.8	379	2	Q6T8N5	Q6t8n5 spermophilu
1305	70.5	5.8	696	1	HIL2_ARATH	Q94f08 arabidopsis	1378	70	5.8	379	2	Q6T8P4	Q6t8p4 spermophilu
1306	70.5	5.8	702	1	S1B3_HUMAN	Q9npd5 h solute ca	1379	70	5.8	379	2	Q6T8R3	Q6t8r3 spermophilu
1307	70.5	5.8	702	1	Q7Z454	Q7z454 homo sapien	1380	70	5.8	379	2	Q6XVQ5	Q6xvy5 proechimys
1308	70.5	5.8	760	1	YCE5_YEAST	P25574 saccharomyc	1381	70	5.8	379	2	Q6XVQ6	Q6xvy6 proechimys
1309	70.5	5.8	773	2	Q963Z5	Q963z5 arabidopsis	1382	70	5.8	379	2	O71FJ0	O71fj0 viverra tan
1310	70.5	5.8	863	2	Q9IV29	Q9iv29 human immu	1383	70	5.8	379	2	Q71FJ1	Q71fj1 viverricula
1311	70.5	5.8	926	2	Q6ZU11	Q6zu11 homo sapien	1384	70	5.8	379	2	Q7Y8L1	Q7y8l1 myotis prui
1312	70.5	5.8	926	2	BAC86416	Bac86416 homo sapi	1385	70	5.8	379	2	Q7YD79	Q7y8l1 pipistrellu
1313	70.5	5.8	1029	2	Q8I252	Q8i252 plasmodium	1386	70	5.8	379	2	Q34814	Q34814 isoethrix bi
1314	70.5	5.8	1075	2	Q49295	Q49295 arabidopsis	1387	70	5.8	379	2	Q35968	Q35968 trinomys al
1315	70.5	5.8	1219	2	Q95XG5	Q95xg5 caenorhabdi	1388	70	5.8	379	2	Q36035	Q36035 trinomys el
1316	70.5	5.8	1449	2	Q8T673	Q8t673 dictyosteli	1389	70	5.8	379	2	Q85B40	Q85b40 mungotictis
1317	70.5	5.8	1583	2	Q9LR38	Q9l1r38 arabidopsis	1390	70	5.8	379	2	Q85PM9	Q85pm9 viverra tan
1318	70.5	5.8	2051	2	Q96682	Q96682 drosophila	1391	70	5.8	379	2	Q85PPI	Q85ppi1 fossa fossa
1319	70.5	5.8	2051	2	Q9V4A7	Q9v4a7 drosophila	1392	70	5.8	379	2	Q8HQE7	Q8hqe7 myotis prui
1320	70.5	5.8	3056	2	Q6PQD5	Q6pqd5 sus scrofa	1393	70	5.8	379	2	Q9T9C0	Q9t9c0 tetraacerus
1321	70.5	5.8	3056	2	AAT01608	Aat01608 sus scrof	1394	70	5.8	379	2	Q9TF29	Q9tf29 spermophilu
1322	70	5.8	185	1	YXEG_BACSTU	P54946 bacillus su	1395	70	5.8	379	2	Q9GGR5	Q9ggr5 proechimys
1323	70	5.8	192	2	Q9RAE3	Q9rae3 rhizobium l	1396	70	5.8	379	2	Q94Y44	Q94y44 tamias stri
1324	70	5.8	210	2	Q92SM9	Q92sm9 rhizobium m	1397	70	5.8	379	2	Q94Y46	Q94y46 tamias sisk
1325	70	5.8	226	1	TMG4_MOUSE	Q8bgn6 mus musculu	1398	70	5.8	379	2	Q94Y67	Q94y67 tamias dors
1326	70	5.8	244	2	Q6HAT0	Q6hat0 bacillus th	1399	70	5.8	379	2	Q8WF61	Q8wff61 sorex caecu
1327	70	5.8	244	2	Q72X94	Q72x94 bacillus ce	1400	70	5.8	379	2	AAH88276	AaH88276 spermophi
1328	70	5.8	244	2	AA544384	Aa544384 bacillus	1401	70	5.8	379	2	AAH88294	AaH88294 spermophi
1329	70	5.8	252	2	Q8AWJ1	Q8awj1 ctenochaetu	1402	70	5.8	379	2	AAH88295	AaH88295 spermophi
1330	70	5.8	253	2	Q6GCV2	Q6gcv2 staphylococ	1403	70	5.8	379	2	AAH88304	AaH88304 spermophi
1331	70	5.8	253	2	Q6GKD2	Q6gkd2 staphylococ	1404	70	5.8	379	2	AAH88305	AaH88305 spermophi
1332	70	5.8	253	2	Q99X47	Q99x47 staphylococ	1405	70	5.8	379	2	AAH88306	AaH88306 spermophi
1333	70	5.8	253	2	Q7A1Y4	Q7a1y4 staphylococ	1406	70	5.8	379	2	AAH88307	AaH88307 spermophi
1334	70	5.8	253	2	Q7A818	Q7a818 staphylococ	1407	70	5.8	379	2	AAH88308	AaH88308 spermophi
1335	70	5.8	253	2	Q8AWK1	Q8awk1 psenopsis a	1408	70	5.8	379	2	AAH88309	AaH88309 spermophi
1336	70	5.8	255	2	Q9XOV6	Q9xov6 neisseria m	1409	70	5.8	379	2	AAH88310	AaH88310 spermophi
1337	70	5.8	258	2	Q94X39	Q94x39 bemisia tab	1410	70	5.8	379	2	AAH88311	AaH88311 spermophi
1338	70	5.8	258	2	Q7MFP97	Q7mf97 vibrio vuln	1411	70	5.8	379	2	AAH88312	AaH88312 spermophi
1339	70	5.8	259	2	Q94X43	Q94x43 bemisia tab	1412	70	5.8	379	2	AAH88313	AaH88313 spermophi
1340	70	5.8	259	2	Q8WA64	Q8wa64 bemisia tab	1413	70	5.8	379	2	AAH88314	AaH88314 spermophi
1341	70	5.8	283	1	LGT_NEIMA	Q9juk4 neisseria m	1414	70	5.8	379	2	AAH88315	AaH88315 spermophi
1342	70	5.8	284	2	Q9DGV8	Q9dgv8 human herpe	1415	70	5.8	379	2	AAH88316	AaH88316 spermophi
1343	70	5.8	284	2	Q9DSE5	Q9des5 human herpe	1416	70	5.8	379	2	AAH88317	AaH88317 spermophi
1344	70	5.8	289	1	OPSD_LIMBE	O42427 limnocottus	1417	70	5.8	379	2	AAH88318	AaH88318 spermophi
1345	70	5.8	290	2	Q6IGA0	O6lga0 photobacter	1418	70	5.8	379	2	AAH88319	AaH88319 spermophi

1419	70	5.8	379	2	AAR88320	Aar88320 spermophi
1420	70	5.8	379	2	AAP42537	Aap42537 proechimy
1421	70	5.8	379	2	AAP42538	Aap42538 proechimy
1422	70	5.8	379	2	AAP42539	Aap42539 proechimy
1423	70	5.8	379	2	AAP42540	Aap42540 proechimy
1424	70	5.8	379	2	AAP42541	Aap42541 proechimy
1425	70	5.8	379	2	AAP42542	Aap42542 proechimy
1426	70	5.8	379	2	AAP42543	Aap42543 proechimy
1427	70	5.8	379	2	AAP42544	Aap42544 proechimy
1428	70	5.8	379	2	AAP42545	Aap42545 proechimy
1429	70	5.8	379	2	AAP42546	Aap42546 proechimy
1430	70	5.8	379	2	AAP42547	Aap42547 proechimy
1431	70	5.8	379	2	AAQ08020	Aaq08020 vivericu
1432	70	5.8	379	2	AAQ08021	Aaq08021 vivera t
1433	70	5.8	380	2	Q7YHK0	Q7yhk0 zoogoneticu
1434	70	5.8	380	2	Q8HNH9	Q8hnh9 myomys dero
1435	70	5.8	381	2	Q7YC71	Q7yc71 apomys grac
1436	70	5.8	398	1	TRFR_SHEEP	Q28596 ovis aries
1437	70	5.8	429	1	ARSB_STAMW	Q8nw09 staphylococ
1438	70	5.8	430	2	Q6Y0P6	Q6y0p6 staphylococ
1439	70	5.8	430	2	AAP32323	Aap32323 staphyloc
1440	70	5.8	432	2	Q8ENQ4	Q8eng4 oceanobacil
1441	70	5.8	435	2	Q6G2S6	Q6g2s6 bartonella
1442	70	5.8	437	2	Q8PRW9	Q8prw9 methanobarc
1443	70	5.8	437	2	Q64811	Q64811 arabidopsis
1444	70	5.8	438	1	CLN3_CANFA	Q29611 canis famli
1445	70	5.8	459	2	Q9G3R4	Q9g3r4 chalinolobu
1446	70	5.8	482	2	Q6T3V7	Q6t3v7 halomonas e
1447	70	5.8	482	2	AAR91792	Aaar91792 halomonas
1448	70	5.8	484	2	Q73RS3	Q73rs3 treponema d
1449	70	5.8	484	2	AAS10510	Aaas10510 treponema
1450	70	5.8	485	2	Q86HV0	Q86hv0 dictyosteli
1451	70	5.8	485	2	Q8NQG2	Q8ngq2 corynebacte
1452	70	5.8	490	1	MOT3_YEAST	P54785 saccharomyc
1453	70	5.8	494	2	Q8EVI8	Q8evi8 mycoplasma
1454	70	5.8	503	2	Q8L6Z8	Q8l6z8 arabidopsi
1455	70	5.8	503	2	AAQ56818	Aaq56818 arabidops
1456	70	5.8	505	2	Q6M5A9	Q6m5a9 corynebacte
1457	70	5.8	505	2	CAF21482	Caft21482 corynebac
1458	70	5.8	507	2	Q9CMF8	Q9cmf8 pasteurella
1459	70	5.8	510	1	ABGT_ECOLI	P46133 escherichia
1460	70	5.8	512	2	Q9ISN6	Q9isn6 neisseria m
1461	70	5.8	514	2	Q9CPB6	Q9cpb6 pasteurella
1462	70	5.8	520	2	Q9SHJ2	Q9shj2 arabidopsis
1463	70	5.8	522	2	Q55340	Q55340 avian infec
1464	70	5.8	557	2	Q9M1E1	Q9m1e1 arabidopsis
1465	70	5.8	559	2	Q8SRA2	Q8sra2 encephalito
1466	70	5.8	578	1	TRM1_DROME	Q9vk89 drosophila
1467	70	5.8	581	2	Q18257	Q18257 caenorhabdi
1468	70	5.8	581	2	CAB16542	Cab16542 caenorhab
1469	70	5.8	607	2	Q6Y4R2	Q6y4r2 cucumaria m
1470	70	5.8	607	2	AAR02393	Aaar02393 cucumaria
1471	70	5.8	668	2	Q9BR66	Q9br66 homo sapien
1472	70	5.8	689	2	Q7JM05	Q7jm05 caenorhabdi
1473	70	5.8	689	2	CAB48501	Caed48501 caenorhab
1474	70	5.8	710	2	Q23383	Q23383 arabidopsis
1475	70	5.8	733	2	Q6BR14	Q6br14 debaryomyce
1476	70	5.8	745	2	Q19870	Q19870 caenorhabdi
1477	70	5.8	745	2	CAA92675	Caag2675 caenorhab
1478	70	5.8	800	2	Q6BUJ9	Q6bjj9 debaryomyce
1479	70	5.8	841	2	Q6KZG3	Q6kzg3 picophilus
1480	70	5.8	853	2	Q7RWS6	Q7rws6 neurospora
1481	70	5.8	857	2	Q73351	Q73351 human immun
1482	70	5.8	860	2	Q998E5	Q998e5 human immun
1483	70	5.8	942	2	Q8PO66	Q8pg66 xanthomonas
1484	70	5.8	1034	2	Q8AB07	Q8ab07 bacteroides
1485	70	5.8	1091	1	RHG7_RAT	Q63744 r rho-gtpas
1486	70	5.8	1097	2	Q8T2F8	Q8t2f8 dictyosteli
1487	70	5.8	1748	1	POLR_ELV	P35928 erysimum la
1488	70	5.8	1748	2	AAC80555	Aac80555 erysimum
1489	70	5.8	2049	2	Q25150	Q25150 halocynthia
1490	70	5.8	4060	2	Q9IHZ8	Q9ihz8 gill-associ
1491	69.5	5.7	142	2	Q8HIP9	Q8hip9 brevineura

1492	69.5	5.7	158	2	Q9ZLA6	Q9zla6 helicobacte
1493	69.5	5.7	193	2	Q6W6S5	Q6w6s5 canis faml
1494	69.5	5.7	193	2	AAQ95550	Aaq95550 canis fam
1495	69.5	5.7	210	2	Q8I546	Q8i546 plasmodium
1496	69.5	5.7	210	2	Q738L1	Q738l1 bacillus ce
1497	69.5	5.7	210	2	AAS41301	Aas41301 bacillus
1498	69.5	5.7	231	2	Q8ZSC7	Q8zsc7 anabaena sp
1499	69.5	5.7	243	2	Q8WEL6	Q8wel6 pogonomyrme
1500	69.5	5.7	255	2	Q86BM2	Q86bm2 drosophila

ALIGNMENTS

RESULT 1						
Q6UWS1						
ID	Q6UWS1	PRELIMINARY;	PRT;	229	AA.	
AC	Q6UWS1;					
DT	05-JUL-2004 (TReMBLrel. 27, Created)					
DT	05-JUL-2004 (TReMBLrel. 27, Last sequence update)					
DT	05-JUL-2004 (TReMBLrel. 27, Last annotation update)					
DE	TCCE518.					
GN	ORFNames=UNQ518;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=2287296; PubMed=12975309;					
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,					
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,					
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,					
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,					
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,					
RA	Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,					
RA	Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,					
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,					
RA	Godowski P.;					
RT	"The secreted protein discovery initiative (SPDI), a large-scale					
RT	effort to identify novel human secreted and transmembrane proteins: a					
RT	bioinformatics assessment.";					
RL	Genome Res. 13:2265-2270(2003).					
DR	EMBL; AY358671; AAQ89034.1; -.					
DR	InterPro; IPR008661; L6_membrane.					
DR	Pfam; PF05805; L6_membrane; 1.					
SQ	SEQUENCE 229 AA; 25109 MW; 1718BD342C58C903 CRC64;					
Query Match						
Best Local Similarity 100.0%; Score 1215; DB 2; Length 229;						
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	MTCCGWTSCNGFSLVLLLVNATPLIVSLVEEDQFSONPISCFEWFPGIIGAGL	60			
Db	1	MTCCGWTSCNGFSLVLLLVNATPLIVSLVEEDQFSONPISCFEWFPGIIGAGL	60			
QY	61	MAIPATMSLTARKRACCNRTGMFLSPFSVITVIGALYCMILISIQALLKGPLMCN	120			
Db	61	MAIPATMSLTARKRACCNRTGMFLSPFSVITVIGALYCMILISIQALLKGPLMCN	120			
QY	121	NSNANCERSLKNISDIHESFNLQWFNFSCAPPTGFNKPSTNDTMASGWRASSF	180			
Db	121	NSNANCERSLKNISDIHESFNLQWFNFSCAPPTGFNKPSTNDTMASGWRASSF	180			
QY	181	ENKHLRHFSVFLGLLVGILEVLFGLSQIVIGFLGCLGVSKRRSQIV	229			
Db	181	ENKHLRHFSVFLGLLVGILEVLFGLSQIVIGFLGCLGVSKRRSQIV	229			
RESULT 2						
ID	AAQ89034	PRELIMINARY;	PRT;	229	AA.	
AC	AAQ89034;					

DT 02-MAR-2004 (Tremblrel. 27, Created)  
 DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)  
 DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)  
 DE TCCE518.  
 GN UNQ518.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=12975309;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seshgiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P.;  
 RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
 RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A  
 RT Bioinformatics Assessment."  
 RL Genome Res. 13:2265-2270(2003).  
 DR EMBL; AY358671; AAQ89034.1; -  
 SQ SEQUENCE 229 AA; 25109 MW; 1718ED342C58C903 CRC64;

Query Match 100.0%; Score 1215; DB 2; Length 229;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-99;  
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTCCEGWTSCNGFSLVLLVGLVLAIPLIYSLVEEDQFSQNPISCFEWWPFGIIGAGL 60  
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 DB 1 MTCCEGWTSCNGFSLVLLVGLVLAIPLIYSLVEEDQFSQNPISCFEWWPFGIIGAGL 60  
 QY 61 MAIPATMTSLTARKRACCNRTGMFLSSFFSVITVIGALYCMILISIQALLKGPLMNCNPS 120  
 |||||  
 DB 61 MAIPATMTSLTARKRACCNRTGMFLSSFFSVITVIGALYCMILISIQALLKGPLMNCNPS 120  
 QY 121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSDNTMASGWRASSFHPDSE 180  
 |||||  
 DB 121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSDNTMASGWRASSFHPDSE 180  
 QY 181 ENKRLIHFSVFLGLLVGLILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229  
 |||||  
 DB 181 ENKRLIHFSVFLGLLVGLILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229

RESULT 3  
 Q9H5X9 PRELIMINARY; PRT; 229 AA.  
 AC Q9H5X9;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Hypothetical protein FLJ22800.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ileal mucosa;  
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,  
 RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,  
 RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,  
 RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,  
 RA Isogai T., Sugano S.;  
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK026453; BAB15488.1; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR InterPro; IPR008661; L6\_membrane.

DR Pfam; PF05805; L6\_membrane; 1.  
 SQ SEQUENCE 229 AA; 25103 MW; B7505D2798B34CDF CRC64;  
 Query Match 99.2%; Score 1205; DB 2; Length 229;  
 Best Local Similarity 99.1%; Pred. No. 2.5e-98;  
 Matches 227; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MTCCEGWTSCNGFSLVLLVGLVLAIPLIYSLVEEDQFSQNPISCFEWWPFGIIGAGL 60  
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 DB 1 MTCCEGWTSCNGFSLVLLVGLVLAIPLIYSLVEEDQFSQNPISCFEWWPFGIIGAGL 60  
 QY 61 MAIPATMTSLTARKRACCNRTGMFLSSFFSVITVIGALYCMILISIQALLKGPLMNCNPS 120  
 |||||  
 DB 61 MAIPATMTSLTARKRACCNRTGMFLSSFFSVITVIGALYCMILISIQALLKGPLMNCNPS 120  
 QY 121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSDNTMASGWRASSFHPDSE 180  
 |||||  
 DB 121 NSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSDNTMASGWRASSFHPDSE 180  
 QY 181 ENKRLIHFSVFLGLLVGLILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229  
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 DB 181 ENKRLIHFSVFLGLLVGLILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229

RESULT 4  
 Q9CQY8 PRELIMINARY; PRT; 226 AA.  
 ID Q9CQY8;  
 AC Q9CQY8;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
 DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,  
 DE RIKEN full-length enriched library, clone:5033426G15 product:similar  
 DE to CDNA: FLJ22800 FIS, CLONE KAI1A2630 (Mus musculus 10 day old male  
 DE pancreas cDNA, RIKEN full-length enriched library, clone:1610018J02  
 DE product:similar to CDNA: FLJ22800 FIS, CLONE KAI1A2630).  
 GN Name=1810018J02Rik;  
 GN Mus musculus (Mouse).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;  
 RX MEDLINE=99279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning."  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;  
 RA the FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;  
 RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes."  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus, and Pancreas;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
DR EMBL; AK017195; BAB30629.1; -.
DR EMBL; AK007532; BAB25093.1; -.
DR MGD; MGI:1913511; 1810018L02Rik.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008661; L6_membrane.
DR Pfam; PF05805; L6_membrane; 1.
SQ SEQUENCE 226 AA; 24760 MW; 3FE6BA1C6A335EAD CRC64;

Query Match 76.1%; Score 924.5; DB 2; Length 226;
Best Local Similarity 74.2%; Pred. No. 1.4e-73;
Matches 170; Conservative 27; Mismatches 29; Indels 3; Gaps 2;

QY 1 MTCCEGWTSCNGFSLLVLLLGVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGL 60
DB 1 MTCCEGWTSCNGFSLLILILGVLINCPILGISLVEADSTSQNPISCFEWWFPGIIGAGL 60

QY 61 MAIPATMTSLTARKRACCNRTGMLSPFSFVITVIGALYCMILISIQALLKPLMCNPS 120
DB 61 MAIPATMTSLAARKRACCNKTKGMLSPFSVITVVGAVYCMVLSQLLEGPLICNTQA 120

QY 121 NSNANCEFSLNISDIHSEFNLMQFFNDSCAPPTGFNKPTSNDTMASCGRASSFHPDSE 180
DB 121 NSTVTCESFLKNLSKPFDESEFNLMFNGTCVSPPTDFKNPTINN-MVSNWKIP--NSNSE 177

QY 181 ENKRLIHFSVFLGLLVLGILLEVLFGLSQIVIGLGLCGVSKRRSQIV 229
DB 178 EDRHRIHFHSVFMSLLVGLLELFGLSQILIGLGLCGVSQRSQIV 226

RESULT 5
Q9D3Q0 PRELIMINARY; PRT; 226 AA.
AC Q9D3Q0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
DE RIKEN full-length enriched library, clone:5033430P14 product:similar
DE to cDNA: FLJ22800 FIS, CLONE KAI1A2630.
GN Name=1810018L02Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
DR EMBL; AK017209; BAB30635.1; -.
DR MGD; MGI:1913511; 1810018L02Rik.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008661; L6_membrane.
DR Pfam; PF05805; L6_membrane; 1.
SQ SEQUENCE 226 AA; 24786 MW; 3FE6BA06703344B7 CRC64;

Query Match 75.6%; Score 918.5; DB 2; Length 226;
Best Local Similarity 73.8%; Pred. No. 4.9e-73;
Matches 169; Conservative 27; Mismatches 30; Indels 3; Gaps 2;

QY 1 MTCCEGWTSCNGFSLLVLLLGVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGL 60
DB 1 MTCCEGWTSCNGFSLLILILGVLINCPILGISLVEADSTSQNPISCFEWWFPGIIGAGL 60
```



```
QY 61 MAIPATMTSLTARKRACNNRTGMFLSSFFSVITVIGALYCM.LISIQALLKGPLMGNPS 120
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 MAIPATMTSLARKRACNNKTKGMFLSSLFSVITVGA VYCM.LVSLQALLLEGPLICNTQA 120
QY 121 NSNANCEFSLKNISDIHPESFNLQWFNDSCAPPTGFNKP.TSNDTMA SGWRASSFHPDSE 180
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 NSTVTCESFLKNLSKFPDESFNLLWFNGTGVSP.TDFKNPTINN-MVINWKIP--NSNSE 177
QY 181 ENKRLHFHSVFLGLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 178 EDRHRIHFHSVFM.SLLVGLLELLFGLSQILLIGFLGCLCGVSQRRSQIV 226

RESULT 6
Q9D3R0 PRELIMINARY; PRT; 226 AA.
AC Q9D3R0:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
DE RIKEN full-length enriched library, clone:503405M13 product:similar
DE to cDNA: FLJ22800 FIS, CLONE KAI1A2630.
GN Name=1810018L02R1k;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakeguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Ozawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
```

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RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary and uterus;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Horii F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK017154; BAB30618.1; -
DR MGD; MGI:1913511; 1810018L02R1k.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008661; L6_membrane.
DR Pfam; PF05805; L6_membrane; 1.
SQ SEQUENCE 226 AA; 24714 MW; 9BE6BE5C2D1EDDC0 CRC64;

Query Match 75.1%; Score 912.5; DB 2; Length 226;
Best Local Similarity 73.8%; Pred. No. 1.6e-72;
Matches 169; Conservative 27; Mismatches 30; Indels 3; Gaps 2;

QY 1 MTCCEGWTSCNGFSLVLVLLGVVNAIPLIVSIVEEDQFSQNPISCFEWWPFGIIGAGL 60
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTCCEGWTSCNGFSLILILILGVVINCIPLGISLVEADSTSQNPISCFEWWPFGIIGAGL 60
QY 61 MAIPATMTSLTARKRACNNRTGMFLSSFFSVITVIGALYCM.LISIQALLKGPLMGNPS 120
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 MAIPATMTSLARKRACGNNKTKGMFLSSLFSVITVGA VYCM.LVSLQALLLEGPLICNTQA 120
QY 121 NSNANCEFSLKNISDIHPESFNLQWFNDSCAPPTGFNKP.TSNDTMA SGWRASSFHPDSE 180
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 NSTVTCESFLKNLSKFPDESFNLLWFNGTGVSP.TDFKNPTINN-MVSNWKIP--NSNSE 177
QY 181 ENKRLHFHSVFLGLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV 229
    |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 178 EDRHRIHFHSVFM.SLLVGLLELLFGLSQILLIGFLGCLCGVSQRRSQIV 226

RESULT 7
Q7SYM6 PRELIMINARY; PRT; 197 AA.
ID Q7SYM6:
AC Q7SYM6:
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Tmsf4-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heitel F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
```





Seq	Sequence	197 AA;	20822 MW;	051AEB5ECCE1075C CRC64;
Qy	Query Match	14.0%;	Score 170;	DB 2; Length 197;
Db	Best Local Similarity	26.5%;	Pred. No. 5.3e-07;	
Matches	61; Conservative	32; Mismatches	91; Indels	46; Gaps 77
Qy	3 CCEGWTSCNGFSLLVLLLGVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGITAGLMA	62		
Db	2 CTGKCARCVCGLSLITLCLVCIVANAL-LIVPNGETSWTNTNHLSQLQWLMGFGIGGLMV	60		
Qy	63 IPATMSLTARKR-----ACCNRTGMFLSSFVSIVITVIGALYCMILISIQALLKGPLMCN	117		
Db	61 LCPGIAAVRAGKGCAGCCGAGCCGNCRCMLRSVFSFSAFGVLGAIYCLISVSGAGLRNP----	116		
Qy	118 SPNSNANCFEFLKNIISDIHPESENLQWFENDSCAPPTGFNKPFTSNDTMASGWRASSFHF	177		
Db	117 -----RC-----LMNGEWGYH-----FEDT-AGAYILNRTLW	142		
Qy	178 DSEENKRLIHFSVFLGLLV--GILEVLFGLSQIVIGFLGCLCGVSKRR	225		
Db	143 DRCEAPRRVVPWNVTLFSLVAASCTEIVLCGIQLVNATIGVPCGDCRKK	192		

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RESULT 10
AAH69519
ID AAH69519 PRELIMINARY; PRT; 197 AA.
AC AAH69519;
DT 01-JUN-2004 (TReMBLrel. 27, Created)
DT 01-JUN-2004 (TReMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TReMBLrel. 27, Last annotation update)
DE Transmembrane 4 superfamily member 5.
GN TM4SF5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosnak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC069519, AAH69519.1; -.
ID Transmembrane.
SQ SEQUENCE 197 AA; 20822 MW; 051AEB5ECCE1075C CRC64;

Query Match 14.0%; Score 170; DB 2; Length 197;
Best Local Similarity 26.5%; Pred. No. 5.3e-07;
Matches 61; Conservative 32; Mismatches 91; Indels 46; Gaps 7;

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QY      CCEGWTSNCGFSLLVLLLLGVVLAIPLIVSLVEEDQFSQNPISCFEWWPGIIGAGLMA 62
      1 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      2 CTGCARCACVGLSLITLCLVCIYANAL-LIVPNEGTSWTNTNHLISLOWMLM3GFIGGLMV 60
QY      63 IPATMSLTARKR-----ACCNKRTGMFLSSFVSITVIGALYCMILISIQALLKGPMLCN 117
      : : : : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      61 LCPGIAAVRAGGKCCGAGCCGCRMLRSVFSFAFGVIGAIYCLSVSAGJLRNGP----- 116
QY      118 SPNSNANCEFSLKNISDIHPESFNLQWFENDSCAPPTGFNKPSTNDTMASGWRASSHF 177
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      117 -----RC-----IMNGEWGYH-----FEDT-AGAYLLNRTILW 142
QY      178 DSEENKRLIHFSVFLGLLV--GILEVLFGLSQIVIGFLGCLCGVSKRR 225
      : : : : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      143 DRCEAPRRVPMNVTLFSLTLVAASCLEIVLCGIQLVNATIGVFCEGDRKK 192

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RESULT 11		
CAG33206		
ID CAG33206	PRELIMINARY;	PRT; 197 AA.
AC CAG33206;		
DT 01-JUN-2004	(TREMBLrel. 27,	Created)
DT 01-JUN-2004	(TREMBLrel. 27,	Last sequence update)
DT 01-JUN-2004	(TREMBLrel. 27,	Last annotation update)
DE TM4SF5 protein.		

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;  
RT "Cloning of human full open reading frames in Gateway(TM) system entry  
RT vector (pDONR201).";  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR456925; CA633206.1; -.  
SQ SEQUENCE 197 AA; 20822 MW; 051AE5ECCE1075C CRC64;

Query Match	14.0%;	Score 170;	DB 2;	Length 197;
Best Local Similarity	26.5%;	Pred. No. 5.3e-07;		
Matches 61;	Conservative 32;	Mismatches 91;	Indels 46;	Gaps 7;

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QY      3 CCEGWTSNGFSLVLVLLGLVNLAIPLIVSLVEEDQFSQNDPISCFEWMIPGIIIGAGLMA 62
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2 CTGKCARCVGLSLITLCLVCIVANAL-LIVPGETSWTNTNHSIQVWLMNGFGIGGLMV 60
QY      63 IPATMSLTARKR-----ACCNRTGMFLSFESFVITVIGALYCM.LISQALLKGPLMCN 117
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61 LCPTGAIVRAGKGC CGAGCCGGRCRM LRSVFS SAGVLA IAYCLSVS GAGLNGP ---- 116
QY      118 SPNSNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMSGWRASSFHF 177
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      117 -----RC-----LMNGEMGYH-----FEDT-AGAYILNRTLM 142
QY      178 DSENGKRLIHFSVFLGLLV--GILEVLFGLSQIVIGFLGLCLGVSKRR 225
      | | : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      143 DRCEAPPRVPMNVTLFSLVAASCLEIVLCGQOLVNATIGVFEGDCKRK 192

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RESULT	12		
T4S1_HUMAN			
ID	T4S1_HUMAN	STANDARD;	PRT; 202 AA.
AC	P30408;		
DT	01-APR-1993	(Rel. 25, Created)	
DT	01-APR-1993	(Rel. 25, last sequence update)	
DT	05-JUL-2004	(Rel. 44, last annotation update)	
DE	Transmembrane 4 superfamily member 1 (Tumor-associated antigen L6)		
DE	(Membrane component, surface marker 1) (M3S1).		
GN	Name=TM4SF1; Synonyms=TAL6;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		

OX NCB1\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92228814; PubMed=1565644;  
RA Marken J.S., Schieven G.L., Hellstroem I., Hellstroem K.E., Aruffo A.;  
RT "Cloning and expression of the tumor-associated antigen L6.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:3503-3507(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow, and Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
FAhey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Roderfeldt Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP TOPOLOGY.  
RX MEDLINE=94171760; PubMed=7510285;  
RA Marken J.S., Bajorath J., Edwards C.P., Farr A.G., Schieven G.L.,  
Hellstrom I., Hellstrom K.E., Aruffo A.;  
RT "Membrane topology of the L6 antigen and identification of the protein  
epitope recognized by the L6 monoclonal antibody.";  
RL J. Biol. Chem. 269:7397-7401(1994).  
CC -1- SUBUNIT: Present in high molecular weight complexes in tumor  
cells.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: Highly expressed on lung, breast, colon, and  
ovarian carcinomas. It is also present on some normal cells,  
endothelial cells in particular.  
CC -1- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.  
CC -----  
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M90657; AAA36158.1; -.  
DR EMBL; BC008442; AAH08442.1; -.  
DR EMBL; BC010166; AAH10166.1; -.  
DR PIR; A42926; A42926.  
DR Genew; HGNC:11853; TM4SF1.  
DR MIM; 191155; -  
DR GO; GO:0005887; C:integral to plasma membrane; IDA.  
DR InterPro; IPR008661; L6\_membrane.  
DR Pfam; PF05805; L6\_membrane; 1.  
KW Antigen; Glycoprotein; Transmembrane.  
FT DOMAIN 1 9 Cytoplasmic (Probable).  
FT TRANSMEM 10 30 Probable.  
FT DOMAIN 31 49 Extracellular (Probable).  
FT TRANSMEM 50 70 Probable.  
FT DOMAIN 71 93 Cytoplasmic (Probable).  
FT TRANSMEM 94 114 Probable.  
FT DOMAIN 115 161 Extracellular (Probable).  
FT TRANSMEM 162 182 Probable.

FT DOMAIN 183 202 Cytoplasmic (Probable).  
FT CARBOHYD 129 129 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 159 159 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 202 AA; 21632 MW; 80D82C47902B8CD4 CRC64;  
Query Match 14.0%; Score 170; DB 1; Length 202;  
Best Local Similarity 27.4%; Pred. No. 5.4e-07;  
Matches 62; Conservative 29; Mismatches 77; Indels 58; Gaps 8;  
QY 10 CNGFSLVLLLVGLVLAIPDIVSLVEEDFSQNPISCFEWMFPPIIGAG-LMAIPATM 68  
| | | | | : | | | | : | | | | : | | | | : | |  
DB 9 CIGHSLVGLALLCIAAN-ILLYFPNGETKYASENHLRSFVWFSSGIVGGILMLPAFVF 67  
QY 69 SLTARKKAC-----CNNRTGMFLSSFVSIVTVIGALYCMILISIQALLKGPMLCNSPSN 121  
: | | | | : | | | | : | | | | : | | | | : | |  
DB 68 IGLEQDDCCGCCGHCNCGKRCAMLSVLAALIGIAGSGYCVIYAALGLAEGPLCLDSLGL- 126  
QY 122 SNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPSTNDTMASGWRASSFHPDSE- 180  
| | | | | : | | | | : | | | | : | | | | : | |  
DB 127 -----QW-----NYTFAS--TEGQYLLDTST 145  
QY 181 -----ENKGRHL-IHFSVFLGILLVGLVLEFGLSQIVIGFLCCLG 220  
| | | | | : | | | | : | | | | : | | | | : | |  
DB 146 WSECTEPKRIWEWNVSLFSILLALGIEFIICLIQVINGVIGIGICG 191  
RESULT 13  
CAG33234  
ID CAG33234 PRELIMINARY; PRT; 202 AA.  
AC CAG33234;  
DT 01-JUN-2004 (TrEMBLrel. 27, Created)  
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)  
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)  
DE TM4SF1 protein.  
GN TM4SF1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCB1\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;  
RT "Cloning of human full open reading frames in Gateway(TM) system entry  
RT vector (pDONR201).";  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR456953; CAG33234.1; -.  
SQ SEQUENCE 202 AA; 21632 MW; 80D82C47902B8CD4 CRC64;  
Query Match 14.0%; Score 170; DB 2; Length 202;  
Best Local Similarity 27.4%; Pred. No. 5.4e-07;  
Matches 62; Conservative 29; Mismatches 77; Indels 58; Gaps 8;  
QY 10 CNGFSLVLLLVGLVLAIPDIVSLVEEDFSQNPISCFEWMFPPIIGAG-LMAIPATM 68  
| | | | | : | | | | : | | | | : | | | | : | |  
DB 9 CIGHSLVGLALLCIAAN-ILLYFPNGETKYASENHLRSFVWFSSGIVGGILMLPAFVF 67  
QY 69 SLTARKKAC-----CNNRTGMFLSSFVSIVTVIGALYCMILISIQALLKGPMLCNSPSN 121  
: | | | | : | | | | : | | | | : | | | | : | |  
DB 68 IGLEQDDCCGCCGHCNCGKRCAMLSVLAALIGIAGSGYCVIYAALGLAEGPLCLDSLGL- 126  
QY 122 SNANCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPSTNDTMASGWRASSFHPDSE- 180  
| | | | | : | | | | : | | | | : | | | | : | |  
DB 127 -----QW-----NYTFAS--TEGQYLLDTST 145  
QY 181 -----ENKGRHL-IHFSVFLGILLVGLVLEFGLSQIVIGFLCCLG 220  
| | | | | : | | | | : | | | | : | | | | : | |  
DB 146 WSECTEPKRIWEWNVSLFSILLALGIEFIICLIQVINGVIGIGICG 191  
RESULT 14  
Q8NE91  
ID Q8NE91 PRELIMINARY; PRT; 232 AA.  
AC Q8NE91;

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DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE TM4SF1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034145; AAH34145.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008661; L6_membrane.
DR Pfam; PF05805; L6_membrane; 1.
SQ SEQUENCE 232 AA; 25057 MW; 90FA2DA611801B84 CRC64;

Query Match 14.0%; Score 170; DB 2; Length 232;
Best Local Similarity 27.4%; Pred. No. 6.3e-07;
Matches 62; Conservative 29; Mismatches 77; Indels 58; Gaps 8;

QY 10 CNGSLVLLLVGLVNAIPILVSLVEDQFSQNPISCFEWWFPGIIGALMAIPATM 68
DB 9 CIGHSLVGLALLCIAAN-ILLYFPNGETKXASENHLRFVWFSGIVGGILMLLPAPVF 67
QY 69 SLTARKRAC-----CNRPTGMFLSSFFSVITVIGALYCMILISIALKGPLMCNSPSN 121
DB 68 IGLEQDDCCGCCGHCNCGKRCAMLSVLAALIGIAGSGYCVIQAALGLAEGPLCLDSL 126
QY 122 SNANCEFLKNISDIHPESFNLOWPFNDSCAPPTGFNKPTSDTMASGWRASSFHFDS 180
DB 127 -----QW-----NYTFAS--TEGQYLLDTST 145
QY 181 -----ENKRL-IFSVFLGLLVGLVLEVLFGLSQIVIGFLGICG 220
DB 146 WSECTEPKHIVENWVSLFSLILALGIEFILCLIQVINGVLGICG 191

RESULT 15
Q6DHT3 PRELIMINARY; PRT; 201 AA.
AC Q6DHT3;
DT 01-OCT-2004 (Tremblrel. 28, Created)
DT 01-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 01-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075884; AAH75884.1; -.
KW Hypothetical protein.
SQ SEQUENCE 201 AA; 21415 MW; 62E7CDD6D75A155 CRC64;
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QY 12 GFSLVLLLVGLVNAIPILVSLVEDQFSQNPISCFEWWFPGIIGALMAIPATM 71
DB 11 GLMLPSAFLSIIAN--LILFFPNGEQDLTKNISLQVLMGILGGILFMCPSCAIR 67
QY 72 ARKR-----ACNRPRTGMFLSSFFSVITVIGALYCMILISIALKGPLMCNSPSN 126
DB 68 AGKGCCGAGCCGNCRCMINSVFSSLFVGIVGVCACVAIALAVGP-----KC 116
QY 127 EFSLKNISDIHPESFNLOWPFNDSCAPPTGFNKPTSDTM-ASGWRASSFHFDS 185
DB 117 QV-----EGEIDWKY-----PFEDRKGNSSYLVDKSSWSECIF---PENM-V 154
QY 186 LIHFSVFLGLLVGLVLEVLFGLSQIVIGFLGICGVSRR 225
DB 155 LWHIVLFSILSLALQAVLCVIVVNGCVGICGDCRKR 194
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Search completed: January 24, 2005, 16:00:00  
Job time : 258 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2005, 15:43:07 ; Search time 40 Seconds  
(without alignments)  
550.841 Million cell updates/sec

Title: US-10-063-553-48  
Perfect score: 1215  
Sequence: 1 MTCCEGWTSCNGFSLVLL.....IVIGFLGCLGVSKRSQIV 229

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	170	14.0	202	2 A42926	L6 surface protein
2	166	13.7	197	2 JC6544	tumor-associated a
3	160	13.2	202	2 A53399	L6 antigen - mouse
4	136	11.2	202	2 JC4635	tumor-associated L
5	133	10.9	202	2 JC6205	cell surface anti
6	90.5	7.4	610	2 A85870	probable transport
7	90.5	7.4	610	2 H91025	probable transport
8	90.5	7.4	610	2 B65001	probable transport
9	89.5	7.4	310	2 A81298	formate dehydrogen
10	88.5	7.3	319	2 T33261	hypothetical prote
11	88	7.2	1036	2 A82357	probable multidrug
12	86.5	7.1	891	2 B82495	probable NADH dehy
13	86	7.1	283	2 AC1340	maltoedextrin ABC-t
14	86	7.1	438	2 H64713	Na+/H+-exchanging
15	85.5	7.0	271	2 B82295	prolipoprotein dia
16	85.5	7.0	457	2 T46332	hypothetical prote
17	85	7.0	283	2 A11710	maltoedextrin ABC-t
18	85	7.0	379	2 S58057	ubiquinol-cytochro
19	84.5	7.0	281	2 T51961	ATAF1-like protein
20	84	6.9	286	2 AC0848	iron transport pro
21	84	6.9	438	2 B71805	Na+/H+-exchanging
22	83	6.8	332	2 T33258	hypothetical prote
23	82	6.7	858	2 T08881	prominin - mouse
24	81.5	6.7	494	2 T32644	hypothetical prote
25	81	6.7	254	2 S20741	chitinase (EC 3.2.
26	81	6.7	461	2 T25671	hypothetical prote
27	80	6.6	379	1 S17418	ubiquinol-cytochro
28	80	6.6	721	2 AH3417	lipa protein [limp
29	79.5	6.5	369	2 T24620	hypothetical prote

30	79.5	6.5	558	2 T47505	hypothetical prote
31	79.5	6.5	608	2 AC0798	probable sodium/bu
32	79.5	6.5	1143	2 T10636	hypothetical prote
33	79	6.5	1353	2 JC4279	adenylate cyclase
34	78.5	6.5	363	2 AH2796	hypothetical prote
35	78.5	6.5	363	2 H97575	probable permease
36	78	6.4	309	2 C89831	conserved hypothet
37	78	6.4	1062	2 F83335	RND multidrug effl
38	78	6.4	1062	2 T30830	hypothetical prote
39	78	6.4	1783	2 T37258	probable voltage-d
40	78	6.4	1917	2 C88728	protein C48A7.1 (I
41	77.5	6.4	459	2 T11489	NADH2 dehydrogenas
42	77.5	6.4	459	2 A89785	hexose phosphate t
43	77.5	6.4	500	2 C70175	L-lactate permease
44	77.5	6.4	557	2 JC5487	cellulase (EC 3.2.
45	77	6.3	347	2 T15672	hypothetical prote
46	77	6.3	1032	2 H64100	acridflavine resist
47	77	6.3	1215	2 C84848	hypothetical prote
48	76.5	6.3	379	2 T11505	ubiquinol-cytochro
49	76.5	6.3	451	2 B70792	hypothetical prote
50	76.5	6.3	538	2 T47624	hypothetical prote
51	76.5	6.3	614	2 S78277	dnak-type molecula
52	76	6.3	346	2 T28718	hypothetical prote
53	76	6.3	431	2 AD1237	arsenic efflux pum
54	76	6.3	447	2 D90012	hypothetical prote
55	76	6.3	532	1 E69821	multidrug resistan
56	76	6.3	561	2 T23564	hypothetical prote
57	76	6.3	604	2 T31042	hypothetical prote
58	76	6.3	751	2 T15230	hypothetical prote
59	76	6.3	1011	2 T13669	neuromusculin - fr
60	75.5	6.2	409	2 T11931	ubiquinol-cytochro
61	75.5	6.2	384	2 AG0362	manganese transpor
62	75.5	6.2	476	2 A84454	hypothetical prote
63	75.5	6.2	788	2 S48191	probable ubiquinol
64	75.5	6.2	824	1 S50767	S-receptor kinase
65	75.5	6.2	1106	2 T19948	hypothetical prote
66	75	6.2	373	2 A11832	hypothetical prote
67	75	6.2	379	2 I49399	ubiquinol-cytochro
68	75	6.2	385	2 G82789	permease XF0589 (I
69	75	6.2	581	2 I45971	prolactin receptor
70	75	6.2	1015	2 T15830	hypothetical prote
71	75	6.2	2201	2 A32160	tenascin-C - human
72	74.5	6.1	254	2 S19390	probable membrane
73	74.5	6.1	429	1 B41902	arsenical pump mem
74	74.5	6.1	432	2 A97832	hypothetical prote
75	74.5	6.1	458	2 S23743	tetracycline resis
76	74.5	6.1	468	2 H82321	arginine/ornithine
77	74.5	6.1	618	2 F86149	hypothetical prote
78	74	6.1	379	1 S17406	ubiquinol-cytochro
79	74	6.1	379	2 I49400	ubiquinol-cytochro
80	74	6.1	431	2 A11599	arsenic efflux pum
81	74	6.1	555	2 T47512	probable transport
82	74	6.1	857	2 JC7716	prominin - rat
83	73.5	6.0	380	2 S70594	ubiquinol-cytochro
84	73.5	6.0	387	2 B84721	hypothetical prote
85	73.5	6.0	429	1 C41903	arsenical pump mem
86	73.5	6.0	544	2 C96943	uncharacterized me
87	73	6.0	280	2 D84015	maltoe/maltoedextr
88	73	6.0	298	2 F87570	hypothetical prote
89	73	6.0	379	1 S17413	ubiquinol-cytochro
90	73	6.0	413	2 S01076	hypothetical prote
91	73	6.0	458	1 YTBSTR	aspartate transam
92	73	6.0	458	1 YTSOG	tetracycline resis
93	73	6.0	458	1 YTBUS6	tetracycline resis
94	73	6.0	458	2 JQ1211	tetracycline resis
95	73	6.0	501	2 H89844	hypothetical prote
96	73	6.0	582	2 T05020	L-ascorbate oxidas
97	73	6.0	718	2 A42163	Na+/myo-inositol c
98	73	6.0	1291	1 A28334	protein-tyrosine-p
99	72.5	6.0	215	2 JU0385	hypothetical 22.6k
100	72.5	6.0	215	2 AH1863	hypothetical prote
101	72.5	6.0	275	2 C89858	conserved hypothet
102	72.5	6.0	290	2 T06856	hypothetical prote



103	72.5	6.0	397	2	S49301	AMUL175 protein -	176	70	5.8	520	2	E86200	protein F12K11.18
104	72.5	6.0	575	2	A54861	tenascin - rat (fr	177	70	5.8	544	2	T27444	hypothetical prote
105	72.5	6.0	598	2	T32166	hypothetical prote	178	70	5.8	557	2	T47506	hypothetical prote
106	72.5	6.0	606	2	T27072	hypothetical prote	179	70	5.8	710	2	T71417	hypothetical prote
107	72.5	6.0	616	2	S50998	transporter protei	180	70	5.8	795	2	T21487	hypothetical prote
108	72.5	6.0	904	2	T40072	p Type Copper Atpa	181	70	5.8	1083	2	SS4293	regulator protein
109	72.5	6.0	1267	2	T21340	hypothetical prote	182	70	5.8	1748	1	TJ3155	gencme polypeptid
110	72	5.9	344	2	S42648	photosystem II chl	183	70	5.8	2049	2	T43161	sodium channel pro
111	72	5.9	344	2	AB2306	photosystem II chl	184	70	5.7	158	2	H71902	phosphatidylglycer
112	72	5.9	378	2	S39007	ubiquinol-cytochro	185	69.5	5.7	231	2	AE2537	two-component resp
113	72	5.9	441	2	D90787	hypothetical prote	186	69.5	5.7	283	2	B86902	permease [imported
114	72	5.9	441	2	D64844	hypothetical prote	187	69.5	5.7	347	2	AD3513	channel protein vi
115	72	5.9	441	2	D64844	probable glycosylt	188	69.5	5.7	356	2	T22882	hypothetical prote
116	72	5.9	447	2	B95369	hypothetical prote	189	69.5	5.7	551	2	A87019	protein-export mem
117	72	5.9	475	2	T39486	hypothetical prote	190	69.5	5.7	474	2	A11821	NADH2 dehydrogenas
118	72	5.9	607	2	T26845	hypothetical prote	191	69.5	5.7	638	2	B34285	receptor protein k
119	72	5.9	617	2	T01227	glutathione-regula	192	69.5	5.7	669	2	T08827	cell division prot
120	72	5.9	982	2	E88465	protein B0244.6 (I	193	69.5	5.7	675	2	D85065	nitrous oxide redu
121	72	5.9	1253	2	T21065	hypothetical prote	194	69.5	5.7	702	2	E64250	probable membrane
122	72	5.9	1583	2	S59644	sister chromatid c	195	69.5	5.7	724	2	A42953	probable RND efflu
123	71.5	5.9	363	2	H71335	probable phospho-N	196	69.5	5.7	822	2	S56823	hypothetical prote
124	71.5	5.9	366	2	C64449	cationic amino aci	197	69.5	5.7	1018	2	E83099	tenascin precursor
125	71.5	5.9	386	2	AD0218	flagellar biosynth	198	69.5	5.7	1817	2	T34249	hypothetical prote
126	71.5	5.9	398	2	JN0708	chytotropin-releas	199	69.5	5.7	2019	1	JQ1322	hypothetical prote
127	71.5	5.9	444	2	G70042	multidrug-efflux t	200	69	5.7	202	2	T26214	KRAG protein - mou
128	71.5	5.9	495	2	T12401	NADH2 dehydrogenas	201	69	5.7	216	2	A54305	aquaporin Z - Esch
129	71.5	5.9	581	2	S03540	gene frizzled prot	202	69	5.7	231	2	C64826	transmembrane wate
130	71.5	5.9	784	2	A86676	carbon starvation	203	69	5.7	231	2	A99749	transmembrane wate
131	71.5	5.9	880	2	A11179	cation (calcium) t	204	69	5.7	231	2	E85599	prolipoprotein dia
132	71.5	5.9	1029	2	C97665	multidrug efflux t	205	69	5.7	283	2	C81124	probable membrane
133	71.5	5.9	1029	2	AF2889	acridflavin resista	206	69	5.7	285	2	A10633	hypothetical prote
134	71.5	5.9	1043	2	AB0370	multidrug efflux p	207	69	5.7	300	2	B69072	hypothetical prote
135	71	5.8	344	2	A69507	conserved hypotnet	208	69	5.7	303	2	T31909	hypothetical prote
136	71	5.8	345	2	B90600	hypothetical prote	209	69	5.7	309	2	T34080	hypothetical prote
137	71	5.8	430	2	G89962	hypothetical prote	210	69	5.7	355	2	D71429	hypothetical prote
138	71	5.8	487	2	B72755	probable antibioti	211	69	5.7	371	2	B86489	protein T32E20.25
139	71	5.8	614	2	T29937	hypothetical prote	212	69	5.7	377	2	T11361	ubiquinol-cytochro
140	71	5.8	708	2	T19969	Na+/H+ antiporter	213	69	5.7	397	2	F83385	probable MFS trans
141	71	5.8	712	2	AG1888	hypothetical prote	214	69	5.7	426	2	T20253	hypothetical prote
142	71	5.8	1246	2	C36806	hypothetical prote	215	69	5.7	475	2	T46745	arginine/ornithine
143	70.5	5.8	129	2	S40363	Ig kappa chain - h	216	69	5.7	494	2	A82294	probable carbon st
144	70.5	5.8	141	2	T11270	NADH2 dehydrogenas	217	69	5.7	513	2	B81217	virulence factor M
145	70.5	5.8	229	1	LCBO	prolactin precursor	218	69	5.7	549	2	E70784	cytochrome b homol
146	70.5	5.8	230	2	A95034	conserved hypotnet	219	69	5.7	617	2	T02668	probable receptor
147	70.5	5.8	236	2	A97905	conserved hypotnet	220	69	5.7	622	2	A11453	bacteriophage mino
148	70.5	5.8	239	2	T48120	hypothetical prote	221	69	5.7	678	2	B71308	hypothetical prote
149	70.5	5.8	282	1	SAVL64	middle surface ant	222	69	5.7	692	2	H71494	probable thiol-dis
150	70.5	5.8	352	2	I50047	rhodopsin - Mexica	223	69	5.7	709	2	S75212	come protein - Syn
151	70.5	5.8	374	2	C83078	still frameshift t	224	69	5.7	814	2	T05537	probable serine/th
152	70.5	5.8	379	2	A53077	ubiquinol-cytochro	225	69	5.7	829	2	B86467	hypothetical prote
153	70.5	5.8	420	2	T47998	peccinacetylastera	226	69	5.7	882	2	AH1536	cation (calcium) t
154	70.5	5.8	446	2	T35005	probable integral	227	69	5.7	971	2	S50912	probable membrane
155	70.5	5.8	477	2	A87285	phosphate ABC tran	228	69	5.7	1852	2	A37860	calcium channel pr
156	70.5	5.8	506	2	F83369	hypothetical prote	229	68.5	5.6	176	2	I53630	cell surface glyco
157	70.5	5.8	522	2	B81584	conserved hypotnet	230	68.5	5.6	269	2	I54432	MHC class II histo
158	70.5	5.8	591	2	C86538	hypothetical prote	231	68.5	5.6	306	2	D90670	hypothetical prote
159	70.5	5.8	591	2	B72086	hypothetical prote	232	68.5	5.6	306	2	G85520	hypothetical prote
160	70.5	5.8	594	2	G84441	probable sucrose-p	233	68.5	5.6	361	2	T45918	hypothetical prote
161	70.5	5.8	760	2	S19374	probable membrane	234	68.5	5.6	369	2	I64234	hypothetical prote
162	70.5	5.8	1056	2	A53767	mucin MUC5B, trach	235	68.5	5.6	374	2	T09771	competence locus E
163	70.5	5.8	1583	2	F86366	protein F26F24.8 [	236	68.5	5.6	379	1	S43262	ubiquinol-cytochro
164	70.5	5.8	2051	2	T13164	plexin B - fruit f	237	68.5	5.6	426	1	SAVLC	large surface anti
165	70	5.8	185	2	A70075	hypothetical prote	238	68.5	5.6	443	2	C70818	probable ABC trans
166	70	5.8	253	2	B89779	hypothetical prote	239	68.5	5.6	452	1	D69810	phosphotransferase
167	70	5.8	255	2	B81197	hypothetical prote	240	68.5	5.6	454	2	AC1413	PTS system, celllob
168	70	5.8	283	2	E81895	probable prolipopr	241	68.5	5.6	469	2	AB1789	permease, multidu
169	70	5.8	379	1	S17419	ubiquinol-cytochro	242	68.5	5.6	511	2	C90446	extreme acid resis
170	70	5.8	379	2	I48180	ubiquinol-cytochro	243	68.5	5.6	511	2	G64902	acid sensitivity p
171	70	5.8	379	2	S58460	ubiquinol-cytochro	244	68.5	5.6	511	2	A90891	acid sensitivity p
172	70	5.8	437	2	E84619	probable serine ca	245	68.5	5.6	511	2	H85726	NADH2 dehydrogenas
173	70	5.8	490	2	S52830	HMS1 protein - yea	246	68.5	5.6	627	2	T11125	hypothetical prote
174	70	5.8	510	2	C64883	membrane protein Y	247	68.5	5.6	643	2	C90035	hypothetical prote
175	70	5.8	512	2	E81794	probable inner mem	248	68.5	5.6	646	2	JQ2150	B went mating prot

249	68.5	5.6	1016	2	F82159	transporter, AcrB/	322	67	5.5	408	2	S37553	triase phosphate/3
250	68.5	5.6	1091	2	G59435	DLC-1 (deleted in	323	67	5.5	411	2	I56444	thyrotrophin-relea
251	68.5	5.6	1500	2	T03824	probable immediate	324	67	5.5	411	2	T17653	hypothetical prote
252	68	5.6	206	2	S08632	nodulin-21 - soybe	325	67	5.5	412	2	S23436	thyroliberin recep
253	68	5.6	228	2	C82400	TonB system transp	326	67	5.5	428	2	S61186	glutamate 5-kinase
254	68	5.6	312	2	G69423	branched-chain ami	327	67	5.5	448	2	C96542	hypothetical prote
255	68	5.6	379	1	S17405	ubiquinol-cytochro	328	67	5.5	454	2	E85826	probable amino aci
256	68	5.6	379	1	S17409	ubiquinol-cytochro	329	67	5.5	454	2	H90980	probable amino aci
257	68	5.6	379	2	I48133	ubiquinol-cytochro	330	67	5.5	462	2	E64966	hypothetical prote
258	68	5.6	379	2	S58451	ubiquinol-cytochro	331	67	5.5	486	2	S42372	amino acid permeas
259	68	5.6	379	2	S58447	ubiquinol-cytochro	332	67	5.5	518	2	S61920	hypothetical prote
260	68	5.6	405	2	T44249	transport protein	333	67	5.5	526	2	T23779	hypothetical prote
261	68	5.6	423	2	S74046	probable sugar tra	334	67	5.5	536	2	A71491	probable integrat
262	68	5.6	425	2	G91082	probable transport	335	67	5.5	537	2	H88087	protein B0454.4 [1
263	68	5.6	425	2	H85927	probable transport	336	67	5.5	537	2	G96598	protein F20N2.6 [1
264	68	5.6	425	2	C65059	probable transport	337	67	5.5	554	2	G97784	hypothetical prote
265	68	5.6	443	2	E65008	hypothetical prote	338	67	5.5	602	2	G97784	hypothetical prote
266	68	5.6	448	2	B82171	probable sodium-de	339	67	5.5	630	2	S46740	NADH2 dehydrogenas
267	68	5.6	465	2	B71716	transhydrogenase c	340	67	5.5	637	2	S01509	probable membrane
268	68	5.6	498	2	A48203	interleukin-14 pre	341	67	5.5	685	2	S67146	probable membrane
269	68	5.6	504	2	S00390	Ig gamma chain (cl	342	67	5.5	792	2	G84830	probable potassium
270	68	5.6	510	2	E97307	probable cardiolip	343	67	5.5	992	2	S49835	hypothetical prote
271	68	5.6	516	2	F82070	2-isopropylmalate	344	67	5.5	2958	2	S64921	probable membrane
272	68	5.6	527	2	H85135	hypothetical prote	345	66.5	5.5	229	1	LCPG	prolactin precursor
273	68	5.6	610	2	H83165	probable sodium/su	346	66.5	5.5	234	2	T11914	coxl intron protei
274	68	5.6	641	2	S44253	raffinose carrier	347	66.5	5.5	268	2	C71872	hypothetical prote
275	68	5.6	689	2	D85013	hypothetical prote	348	66.5	5.5	319	2	AF0489	probable iron tran
276	68	5.6	725	2	B82425	conserved hypotet	349	66.5	5.5	407	2	A69188	ammonium transport
277	68	5.6	799	2	A48716	glycine transporte	350	66.5	5.5	410	2	C64618	conserved hypotet
278	68	5.6	865	2	B96558	probable protein k	351	66.5	5.5	482	2	T02538	hypothetical prote
279	68	5.6	926	2	T16184	hypothetical prote	352	66.5	5.5	489	2	B69833	metabolite permeas
280	68	5.6	1008	1	GNVUTK	glycoprotein precu	353	66.5	5.5	489	2	T24971	hypothetical prote
281	68	5.6	1247	2	C89583	protein K07E3.1 [1	354	66.5	5.5	705	2	S23352	gene unc-93 protei
282	68	5.6	1810	1	A32230	tenascin precursor	355	66.5	5.5	719	2	T00266	hypothetical prote
283	68	5.6	3176	2	CGHU3A	collagen alpha 3(V	356	66.5	5.5	937	2	A56517	nucleoporin Nup98
284	67.5	5.6	120	2	A11727	hypothetical prote	357	66.5	5.5	1078	2	A56715	calcium receptor (
285	67.5	5.6	197	2	B69447	hypothetical prote	358	66.5	5.5	1088	2	B56715	calcium receptor (
286	67.5	5.6	208	2	E97899	hypothetical prote	359	66.5	5.5	3391	1	GNMV16	genome polypeptid
287	67.5	5.6	228	2	T16678	hypothetical prote	360	66.5	5.5	4981	2	T18489	23K integral prote
288	67.5	5.6	229	1	LCSH	prolactin precursor	361	66	5.4	218	1	A43522	hypothetical prote
289	67.5	5.6	261	2	I68718	MHC class II histo	362	66	5.4	222	2	F64563	Bola-DQ beta-1 - b
290	67.5	5.6	328	1	S25993	NADH2 dehydrogenas	363	66	5.4	238	2	A45544	probable membrane
291	67.5	5.6	337	2	B88957	protein ZK697.7 [1	364	66	5.4	239	2	S64327	conserved hypotet
292	67.5	5.6	379	2	S58458	ubiquinol-cytochro	365	66	5.4	255	2	F81833	hypothetical prote
293	67.5	5.6	386	2	G84386	oligopeptide trans	366	66	5.4	271	2	AC1692	hypothetical prote
294	67.5	5.6	415	2	B84858	hypothetical prote	367	66	5.4	295	2	C70166	hypothetical prote
295	67.5	5.6	431	1	SAVL59	large surface anti	368	66	5.4	339	2	T22195	platelet-activatin
296	67.5	5.6	431	2	F90316	dsrf protein, prob	369	66	5.4	342	2	A40191	hemn permease Uvj
297	67.5	5.6	452	2	G95306	putrescine/ornithi	370	66	5.4	348	2	E82896	thyrotropin releas
298	67.5	5.6	456	2	H96902	membrane protein,	371	66	5.4	352	2	JB0296	hypothetical prote
299	67.5	5.6	472	2	T29313	hypothetical prote	372	66	5.4	373	2	S54545	ubiquinol-cytochro
300	67.5	5.6	491	2	G90689	regulates beta-lac	373	66	5.4	379	1	CBBO	ubiquinol-cytochro
301	67.5	5.6	491	2	C85540	signal transducer	374	66	5.4	379	2	T11259	ubiquinol-cytochro
302	67.5	5.6	491	2	S37391	probable membrane	375	66	5.4	381	1	CBMS	ubiquinol-cytochro
303	67.5	5.6	509	2	T25401	hypothetical prote	376	66	5.4	383	2	S54213	flagellar biosynth
304	67.5	5.6	548	2	T38541	probable sucrose c	377	66	5.4	402	2	T29703	hypothetical prote
305	67.5	5.6	553	2	T31884	hypothetical prote	378	66	5.4	413	2	H82270	hypothetical prote
306	67.5	5.6	656	2	T31884	G protein-coupled	379	66	5.4	414	2	S34829	triase phosphate/3
307	67.5	5.6	907	2	JG0193	hypothetical prote	380	66	5.4	414	2	S23224	triase phosphate/3
308	67.5	5.6	955	2	T21612	probable mmp12 pro	381	66	5.4	422	2	D72302	hypothetical prote
309	67.5	5.6	968	2	F70746	multidrug efflux p	382	66	5.4	444	2	S62414	hypothetical prote
310	67.5	5.6	1041	2	AC0423	voltage-dependent	383	66	5.4	447	2	AI0701	probable ubiquitin
311	67.5	5.6	1610	2	A46227	calcium channel al	384	66	5.4	482	2	A39285	calcitonin recepto
312	67.5	5.6	2161	2	JH0564	calcium channel al	385	66	5.4	498	2	I47130	calcitonin recepto
313	67.5	5.6	2181	2	A38198	hypothetical prote	386	66	5.4	505	2	F90427	amino acid transpo
314	67	5.5	252	2	A86449	conserved hypotet	387	66	5.4	581	2	S17150	potassium channel
315	67	5.5	296	2	AH1173	hypothetical prote	388	66	5.4	583	2	A25096	NADH2 dehydrogenas
316	67	5.5	314	2	T15519	6a-hydroxymaackiai	389	66	5.4	598	2	B70036	capsular polysacch
317	67	5.5	360	2	T06786	ubiquinol-cytochro	390	66	5.4	609	2	T11310	NADH2 dehydrogenas
318	67	5.5	379	1	S17420	ubiquinol-cytochro	391	66	5.4	611	2	S09142	NDS intron 1 prote
319	67	5.5	379	2	S58085	thyrotropin-releas	392	66	5.4	650	2	S23217	beta-fructofuranos
320	67	5.5	393	2	A39251	triase phosphate/3	393	66	5.4	674	2	T21217	hypothetical prote
321	67	5.5	407	2	S37550		394	66	5.4				

395	66	5.4	689	2	T11917	NADH2 dehydrogenas
396	66	5.4	718	2	A56851	Na+/myo-inositol c
397	66	5.4	754	2	A11627	protein-export mem
398	66	5.4	770	2	S60676	cellobiose oxidase
399	66	5.4	877	2	C46356	env polyprotein -
400	66	5.4	893	2	S64926	probable membrane
401	66	5.4	1034	2	D65119	acriflavin resista
402	66	5.4	1217	2	T00270	hypothetical prote
403	66	5.4	1218	2	T30293	ABC transport prot
404	66	5.4	1615	2	JE0372	low density lipopr
405	65.5	5.4	83	2	AG3378	hypothetical membr
406	65.5	5.4	139	2	G32536	T-cell receptor al
407	65.5	5.4	226	1	JX0221	CD9 antigen - bovi
408	65.5	5.4	229	2	A61133	prolactin precursor
409	65.5	5.4	233	2	H82944	thymidylate kinase
410	65.5	5.4	258	2	A29088	Smh class II histo
411	65.5	5.4	259	2	S64423	probable membrane
412	65.5	5.4	261	1	HLHUD8	MHC class II histo
413	65.5	5.4	277	2	D42400	membrane protein M
414	65.5	5.4	279	2	AB1745	conserved hypothet
415	65.5	5.4	279	2	AD1375	conserved hypothet
416	65.5	5.4	293	1	QOCVBV	BL1 protein - aqua
417	65.5	5.4	342	2	AD2367	hypothetical prote
418	65.5	5.4	361	2	T21529	hypothetical prote
419	65.5	5.4	379	1	S43261	ubiquinol-cytochro
420	65.5	5.4	379	1	S43265	ubiquinol-cytochro
421	65.5	5.4	379	1	S43269	ubiquinol-cytochro
422	65.5	5.4	379	2	S58459	ubiquinol-cytochro
423	65.5	5.4	380	1	S73751	high affinity tran
424	65.5	5.4	405	2	C71462	hypothetical prote
425	65.5	5.4	435	2	AC0104	probable sugar tra
426	65.5	5.4	529	2	T22398	hypothetical prote
427	65.5	5.4	530	1	A56841	glucose-6-phosphat
428	65.5	5.4	534	2	A37483	F protein - Muraya
429	65.5	5.4	587	2	D84426	hypothetical prote
430	65.5	5.4	620	2	T49067	transcription fact
431	65.5	5.4	656	2	B49423	semaphorin I - fru
432	65.5	5.4	806	2	C86445	hypothetical prote
433	65.5	5.4	856	1	A44963	env polyprotein pr
434	65.5	5.4	868	2	T31527	hypothetical prote
435	65.5	5.4	897	2	S67283	hypothetical prote
436	65.5	5.4	910	2	C69069	cation-transportin
437	65.5	5.4	928	2	S50578	hypothetical prote
438	65.5	5.4	1029	2	D83120	probable RND efflu
439	65.5	5.4	1085	2	S40476	Ca(2+)-sensing rec
440	65.5	5.4	1246	2	T00826	hypothetical prote
441	65.5	5.4	1623	2	T01369	ABC transporter At
442	65.5	5.4	1737	2	T17101	probable voltage-a
443	65.5	5.4	1816	2	A84845	probable ABC trans
444	65.5	5.4	2163	2	T15276	hypothetical prote
445	65	5.3	136	2	S05628	NADH2 dehydrogenas
446	65	5.3	172	2	B82464	probable acetyltra
447	65	5.3	203	2	F91006	hypothetical prote
448	65	5.3	212	2	A12032	hypothetical prote
449	65	5.3	271	2	AH0161	probable membrane
450	65	5.3	301	2	C69143	hypothetical prote
451	65	5.3	336	2	B64717	methicillin resist
452	65	5.3	338	2	S50339	NADH2 dehydrogenas
453	65	5.3	365	2	AE2782	transcription regu
454	65	5.3	365	2	F97561	hypothetical prote
455	65	5.3	373	2	G85355	nodulin-like prote
456	65	5.3	379	1	S41832	ubiquinol-cytochro
457	65	5.3	379	1	S43263	ubiquinol-cytochro
458	65	5.3	379	2	I48134	ubiquinol-cytochro
459	65	5.3	379	2	S58452	ubiquinol-cytochro
460	65	5.3	379	2	S58851	ubiquinol-cytochro
461	65	5.3	379	2	S58448	ubiquinol-cytochro
462	65	5.3	389	2	B96522	ubiquinol-cytochro
463	65	5.3	400	2	B82367	hypothetical prote
464	65	5.3	423	2	C84176	probable multidrug
465	65	5.3	423	2	AG2394	oxalate/formate an
466	65	5.3	455	2	T16070	hypothetical prote
467	65	5.3	473	2	S51256	hypothetical prote
468	65	5.3	487	2	C82215	probable transport
469	65	5.3	509	2	A33801	muscle-fat glucose
470	65	5.3	563	2	T44214	probable phosphotr
471	65	5.3	563	2	T44029	ganciclovir kinase
472	65	5.3	580	2	A56382	purine permease, b
473	65	5.3	616	2	T03027	receptor-like prot
474	65	5.3	652	2	H96924	probable phosphohy
475	65	5.3	667	2	S51763	sulfate transport
476	65	5.3	728	2	C75601	cation-transportin
477	65	5.3	754	2	AG1265	protein-export mem
478	65	5.3	826	2	B81706	conserved hypothet
479	65	5.3	1018	1	GNMXG7	genome polyprotein
480	65	5.3	1042	2	I50099	H,K-ATPase - giant
481	65	5.3	1106	2	T25065	hypothetical prote
482	65	5.3	1219	2	T06608	disease resistance
483	65	5.3	1231	2	E90182	hypothetical prote
484	65	5.3	2195	2	T34264	hypothetical prote
485	64.5	5.3	125	2	JH0184	hydrophobin Sc3 pr
486	64.5	5.3	154	2	T18204	mxhB protein - Bac
487	64.5	5.3	163	2	B84731	hypothetical prote
488	64.5	5.3	191	2	AD2040	hypothetical prote
489	64.5	5.3	197	2	B81720	conserved hypothet
490	64.5	5.3	218	2	G71260	probable ribulose-
491	64.5	5.3	218	2	F81111	nickal-dependent h
492	64.5	5.3	220	2	D71946	hypothetical prote
493	64.5	5.3	229	2	I83982	prolactin - goat
494	64.5	5.3	247	2	I45942	MHC class II - bov
495	64.5	5.3	253	2	B34801	pathogenesis-relat
496	64.5	5.3	261	2	I45928	MHC class II - bov
497	64.5	5.3	305	2	S29711	olfactory factor O
498	64.5	5.3	321	2	A10007	lipopolysaccharide
499	64.5	5.3	322	2	C83562	hypothetical prote
500	64.5	5.3	326	2	G84748	hypothetical prote
501	64.5	5.3	330	2	T43061	hypothetical prote
502	64.5	5.3	331	1	DN0BU1	NADH2 dehydrogenas
503	64.5	5.3	331	2	F89771	lipoprotein limpor
504	64.5	5.3	340	2	E83126	ferric enterobacti
505	64.5	5.3	346	2	AH3563	ribose transport s
506	64.5	5.3	372	2	AG1834	NADH dehydrogenase
507	64.5	5.3	379	1	S43266	ubiquinol-cytochro
508	64.5	5.3	379	1	S43268	ubiquinol-cytochro
509	64.5	5.3	379	2	S58466	ubiquinol-cytochro
510	64.5	5.3	385	2	I84455	ubiquinol-cytochro
511	64.5	5.3	393	2	A64036	dopamine transport
512	64.5	5.3	402	2	A84581	hypothetical prote
513	64.5	5.3	431	1	SAVL7	probable disease r
514	64.5	5.3	431	1	SAVLW8	large surface anti
515	64.5	5.3	435	2	C96759	arsenical pump mem
516	64.5	5.3	441	2	C96759	protein serine car
517	64.5	5.3	443	2	T20292	hypothetical prote
518	64.5	5.3	454	2	AG0763	probable amino aci
519	64.5	5.3	464	2	T50785	nucleoid DNA-bindi
520	64.5	5.3	503	2	T38303	SWI/SNF complex tr
521	64.5	5.3	512	2	G90399	amino acid transpo
522	64.5	5.3	561	2	A11409	potassium-transport
523	64.5	5.3	574	2	T41068	hypothetical prote
524	64.5	5.3	620	2	I57937	dopamine transport
525	64.5	5.3	620	2	A48980	dopamine transport
526	64.5	5.3	634	2	T22351	hypothetical prote
527	64.5	5.3	659	2	H96693	hypothetical prote
528	64.5	5.3	683	2	T03146	probable glycoprot
529	64.5	5.3	689	1	E70408	ferrous iron trans
530	64.5	5.3	724	2	D84377	protein export lim
531	64.5	5.3	803	2	S45916	hypothetical prote
532	64.5	5.3	879	2	D96902	MDR-type permease
533	64.5	5.3	958	2	A70634	probable mmp1 pro
534	64.5	5.3	1028	2	AD0052	probable multi-dru
535	64.5	5.3	1135	1	JQ1928	G2-G: polyprotein
536	64.5	5.3	1150	2	AB0064	probable membrane
537	64.5	5.3	1165	1	S45879	chitin synthase (E
538	64.5	5.3	1447	1	VGJHE3	E2 g:ycoprotein pr
539	64.5	5.3	1447	1	VGJHE2	E2 g:ycoprotein pr
540	64.5	5.3	1487	2	S62048	probable membrane

541	64.5	5.3	1495	2	E86428	probable ABC trans	614	63.5	5.2	308	2	T24453	hypothetical prote
542	64.5	5.3	1646	2	JH0422	voltage-dependent	615	63.5	5.2	350	2	C88987	protein C50H11.2 f
543	64.5	5.3	1687	2	T30244	phosphodiesterase	616	63.5	5.2	351	2	T23990	hypothetical prote
544	64.5	5.3	1719	2	T30174	exoribonuclease, v	617	63.5	5.2	367	2	C82943	ferriochrome ABC tr
545	64.5	5.3	1748	1	JN0786	integrin beta-4 ch	618	63.5	5.2	379	1	S17415	ubiquinol-cytochro
546	64.5	5.3	2203	2	T42742	voltage-dependent	619	63.5	5.2	379	2	T11492	ubiquinol-cytochro
547	64.5	5.3	2262	2	T30890	calcium channel al	620	63.5	5.2	379	2	T10998	ubiquinol-cytochro
548	64	5.3	159	2	G75555	conserved hypothet	621	63.5	5.2	385	2	H71960	hypothetical prote
549	64	5.3	167	2	I58352	p16INK4a - mouse	622	63.5	5.2	387	2	F82692	conserved hypothet
550	64	5.3	227	2	F96777	germin-like protei	623	63.5	5.2	389	2	H86266	hypothetical prote
551	64	5.3	232	2	S32398	serine proteinase	624	63.5	5.2	442	2	H81402	probable integral
552	64	5.3	253	2	AE2797	cytochrome c-type	625	63.5	5.2	446	2	H90094	hypothetical prote
553	64	5.3	254	2	A64728	probable membrane	626	63.5	5.2	454	2	H91127	L-serine deaminase
554	64	5.3	261	2	T11486	cytochrome-c oxida	627	63.5	5.2	456	2	G85972	probable L-serine
555	64	5.3	267	2	E97576	cytochrome c-type	628	63.5	5.2	458	1	Y7BSY8	tetracycline resis
556	64	5.3	318	2	AH0499	probable phosphat	629	63.5	5.2	463	2	D69792	amino acid permeas
557	64	5.3	333	2	T02614	hypothetical prote	630	63.5	5.2	508	2	T21866	hypothetical prote
558	64	5.3	335	2	B71801	probable undecapre	631	63.5	5.2	521	2	C86678	hypothetical prote
559	64	5.3	350	2	E81303	probable branched-	632	63.5	5.2	522	2	T29705	hypothetical prote
560	64	5.3	355	1	A46191	iodopsin homolog -	633	63.5	5.2	531	2	T19232	hypothetical prote
561	64	5.3	357	2	C69223	anion permease - M	634	63.5	5.2	532	2	T52442	hypothetical prote
562	64	5.3	378	2	D64181	probable cytochrom	635	63.5	5.2	561	2	AH1785	potassium-transpor
563	64	5.3	379	1	S17407	ubiquinol-cytochro	636	63.5	5.2	568	2	T31692	hypothetical prote
564	64	5.3	379	2	S58461	ubiquinol-cytochro	637	63.5	5.2	596	2	T17333	hypothetical prote
565	64	5.3	379	2	T11349	ubiquinol-cytochro	638	63.5	5.2	608	2	AG0846	hypothetical prote
566	64	5.3	382	2	A72373	conserved hypothet	639	63.5	5.2	610	2	F82192	formate hydrogently
567	64	5.3	396	2	F96545	hypothetical prote	640	63.5	5.2	621	2	AF3016	ABC transporter. A
568	64	5.3	405	2	A57479	amino acid transpo	641	63.5	5.2	642	2	B98268	Na <sup>+</sup> /H <sup>+</sup> antiporter
569	64	5.3	426	2	E71675	hypothetical prote	642	63.5	5.2	696	2	T48432	probable sodium/hy
570	64	5.3	428	2	T33775	hypothetical prote	643	63.5	5.2	698	2	T10541	matutase-like prot
571	64	5.3	444	2	JC1141	metacyclic-form-sp	644	63.5	5.2	741	2	S73827	hypothetical prote
572	64	5.3	445	2	A70732	hypothetical prote	645	63.5	5.2	776	2	T50299	hypothetical serin
573	64	5.3	447	2	T13204	hypothetical prote	646	63.5	5.2	776	2	T20896	hypothetical prote
574	64	5.3	457	2	T39751	major facilitator	647	63.5	5.2	845	2	D97163	cation transport P
575	64	5.3	461	2	T11800	NADH2 dehydrogenas	648	63.5	5.2	936	2	T26521	hypothetical prote
576	64	5.3	466	2	G71542	probable amino aci	649	63.5	5.2	1050	2	AE0380	multidrug efflux p
577	64	5.3	470	2	AD1430	transmembrane effl	650	63.5	5.2	1103	2	T42022	probable chitin sy
578	64	5.3	492	2	S59107	NADH2 dehydrogenas	651	63.5	5.2	1142	2	S59359	GIN4 protein - yea
579	64	5.3	565	2	E90113	probable membrane	652	63.5	5.2	1220	2	S64916	probable membrane
580	64	5.3	692	2	T16408	hypothetical prote	653	63.5	5.2	1604	2	B86287	P9L1.23 protein -
581	64	5.3	768	2	T22758	hypothetical prote	654	63.5	5.2	1612	2	S51243	probable ATPase (E
582	64	5.3	798	2	T23539	hypothetical prote	655	63.5	5.2	2143	2	JH0427	voltage-dependent
583	64	5.3	810	2	T33323	hypothetical prote	656	63.5	5.2	3388	1	GNMWDP	genome polypeptid
584	64	5.3	953	2	T01093	luminidependens pr	657	63	5.2	115	2	G97022	probable membrane
585	64	5.3	970	2	F64230	spore germination	658	63	5.2	134	2	S40376	probable membrane
586	64	5.3	992	2	A42318	glycogen phosphory	659	63	5.2	217	2	F83840	Ig kappa chain - h
587	64	5.3	996	2	A95228	bacteriocin format	660	63	5.2	218	1	A40181	stage II sporulacti
588	64	5.3	996	2	E98092	cyLM protein, cyto	661	63	5.2	232	2	B90129	23K integral membr
589	64	5.3	1174	2	A39927	RNA-directed RNA p	662	63	5.2	239	2	S66341	26S proteasome SU
590	64	5.3	1182	2	T13952	membrane protein p	663	63	5.2	239	2	F64382	hypothetical prote
591	64	5.3	1280	2	A39117	170K lectin precur	664	63	5.2	251	2	H90568	conserved hypothet
592	64	5.3	1297	2	T39287	hypothetical prote	665	63	5.2	254	2	B90637	hypothetical prote
593	64	5.3	1689	2	S72467	sodium channel pro	666	63	5.2	254	2	E85488	hypothetical prote
594	64	5.3	2787	2	S45416	TELI protein - yea	667	63	5.2	257	2	A32283	MHC class II histo
595	63.5	5.2	115	2	AB2223	hypothetical prote	668	63	5.2	260	2	A34178	bacteriorhodopsin
596	63.5	5.2	145	2	T42280	hypothetical prote	669	63	5.2	271	2	AC1320	hypothetical prote
597	63.5	5.2	158	2	I61900	eosinophil prote	670	63	5.2	276	2	F72342	conserved hypothet
598	63.5	5.2	171	2	I48085	integral membrane	671	63	5.2	292	2	T19669	hypothetical prote
599	63.5	5.2	219	2	I45937	MHC cell surface g	672	63	5.2	292	2	G88783	hypothetical prote
600	63.5	5.2	253	2	S20737	chitinase (EC 3.2.	673	63	5.2	295	2	A41241	protein C33A12.16
601	63.5	5.2	253	2	S20738	chitinase (EC 3.2.	674	63	5.2	309	2	AC0489	ubiquitin-conjugat
602	63.5	5.2	261	1	HLHUI C	MHC class II histo	675	63	5.2	313	2	S66962	probable membrane
603	63.5	5.2	261	2	I55996	MHC HLA-DQ-beta ce	676	63	5.2	314	2	T33862	hypothetical prote
604	63.5	5.2	261	2	B37044	MHC class II histo	677	63	5.2	320	2	T26259	hypothetical prote
605	63.5	5.2	261	2	I68732	MHC class II histo	678	63	5.2	339	2	A81288	probable sugar kin
606	63.5	5.2	261	2	I54480	HLA DQ-beta - huma	679	63	5.2	341	2	S63666	platelet activatin
607	63.5	5.2	261	2	I45943	MHC class II - bov	680	63	5.2	341	2	AE1824	permease protein o
608	63.5	5.2	263	2	T46093	hypothetical prote	681	63	5.2	353	2	A88987	protein C50H11.4 f
609	63.5	5.2	273	2	T49007	hypothetical prote	682	63	5.2	354	2	T20169	hypothetical prote
610	63.5	5.2	275	2	D65100	hypothetical h-ser	683	63	5.2	356	2	G82938	hemin transport sy
611	63.5	5.2	286	2	AI3105	hypothetical prote	684	63	5.2	360	2	F70819	probable ionicttran
612	63.5	5.2	288	2	A90135	SAM-dependent meth	685	63	5.2	376	2	S33654	zinc transport pro
613	63.5	5.2	301	2	C98181	bitc protein (AF12	686	63	5.2	379	2	S58464	ubiquinol-cytochro

687	63	5.2	391	2	H88955	protein K04Fl.2 [i
688	63	5.2	394	2	AC1554	DLTB protein for D
689	63	5.2	400	2	F86887	hypothetical prote
690	63	5.2	418	2	E86395	hypothetical prote
691	63	5.2	429	2	AC0801	probable amino aci
692	63	5.2	430	2	A90313	transport protein
693	63	5.2	433	2	AF1739	PTS system, cellob
694	63	5.2	434	2	T19205	hypothetical prote
695	63	5.2	437	2	H81041	citrate transporte
696	63	5.2	438	2	A64147	hypothetical prote
697	63	5.2	440	2	T24837	hypothetical prote
698	63	5.2	458	2	JS0616	serotonin receptor
699	63	5.2	470	2	AF0771	probable transport
700	63	5.2	493	2	C97853	NADH2 dehydrogenas
701	63	5.2	521	2	B33531	cytochrome P450 2A
702	63	5.2	521	2	T15322	hypothetical prote
703	63	5.2	526	2	C71315	probable virulence
704	63	5.2	532	2	T23481	hypothetical prote
705	63	5.2	533	2	H86282	protein F10B6.34 [
706	63	5.2	556	2	S51892	probable membrane
707	63	5.2	567	2	S58750	NADH2 dehydrogenas
708	63	5.2	600	2	T11889	NADH2 dehydrogenas
709	63	5.2	619	1	KSNCL0	laccase (EC 1.10.3
710	63	5.2	619	1	KSNCLT	probable membrane
711	63	5.2	651	2	AG0448	semaphorin homolog
712	63	5.2	653	2	T03102	sulfate transport
713	63	5.2	662	2	S51764	structural protein
714	63	5.2	681	2	S33316	probable copper-tr
715	63	5.2	745	1	S75354	gene COX1 intron 4
716	63	5.2	763	1	S17998	gene 51 protein -
717	63	5.2	835	1	MZBE51	hypothetical prote
718	63	5.2	870	2	T25338	respiratory burst
719	63	5.2	921	2	T51804	hypothetical prote
720	63	5.2	956	2	T40953	cell division cont
721	63	5.2	974	2	S15038	probable disease r
722	63	5.2	994	2	H96510	hypothetical prote
723	63	5.2	1030	2	T18669	hypothetical prote
724	63	5.2	1043	2	F97302	hypothetical prote
725	63	5.2	1125	1	OYURCP	superact receptor p
726	63	5.2	1194	2	E96624	hypothetical prote
727	63	5.2	1294	2	S77690	probable membrane
728	63	5.2	1430	2	T27924	hypothetical prote
729	63	5.2	1776	1	RRWPYM	genome polyprotein
730	63	5.2	1998	2	T13009	hypothetical prote
731	63	5.2	2809	2	T30213	G-cadherin - sea u
732	62.5	5.1	144	2	S21349	ferredoxin-16.3K
733	62.5	5.1	174	1	RDSPTA	conserved hypotnet
734	62.5	5.1	206	2	D83317	hypothetical prote
735	62.5	5.1	207	2	AG2553	hypothetical prote
736	62.5	5.1	237	2	T05249	hypothetical prote
737	62.5	5.1	249	2	E90048	MHC class II histo
738	62.5	5.1	261	1	HHV2C	class II histocomp
739	62.5	5.1	261	2	B32527	probable hydrolyase
740	62.5	5.1	276	2	H96985	conserved hypotnet
741	62.5	5.1	296	2	A11530	B-cell surface ant
742	62.5	5.1	297	1	A30586	phosphate specific
743	62.5	5.1	301	2	H70584	hypothetical prote
744	62.5	5.1	301	2	C85049	cytochrome-c oxida
745	62.5	5.1	311	2	S66600	conserved hypotnet
746	62.5	5.1	326	2	G89835	hypothetical prote
747	62.5	5.1	327	2	T25780	thymidine kinase (
748	62.5	5.1	350	1	KIBBFC	uncharacterized co
749	62.5	5.1	350	2	D97298	rhodopsin - chicke
750	62.5	5.1	351	2	S29152	efflux protein hom
751	62.5	5.1	394	2	S39739	protein-export mem
752	62.5	5.1	396	1	G64313	hypothetical prote
753	62.5	5.1	397	2	C83470	aspartate transam
754	62.5	5.1	413	2	S29027	cytosine permease
755	62.5	5.1	416	2	E83590	hypothetical prote
756	62.5	5.1	435	2	AI2082	hypothetical prote
757	62.5	5.1	446	2	G72287	conserved hypotnet
758	62.5	5.1	450	2	B81730	hypothetical prote
759	62.5	5.1	465	2	H97712	hypothetical prote
760	62.5	5.1	466	2	T32204	hypothetical prote
761	62.5	5.1	470	2	G97263	PTS system enzyme
762	62.5	5.1	473	2	G90401	flagella-related p
763	62.5	5.1	481	2	T23131	hypothetical prote
764	62.5	5.1	497	2	F86712	di-/tripeptide tra
765	62.5	5.1	502	2	T05135	hypothetical prote
766	62.5	5.1	505	2	AD0511	probable carnitine
767	62.5	5.1	516	2	A84081	hypothetical prote
768	62.5	5.1	522	2	T18504	hypothetical prote
769	62.5	5.1	546	2	D83408	hypothetical prote
770	62.5	5.1	548	2	T47510	probable transport
771	62.5	5.1	617	2	T51917	related to transfo
772	62.5	5.1	638	2	S36546	E1 protein - human
773	62.5	5.1	657	2	A54011	cationic amino aci
774	62.5	5.1	661	2	S37592	beta-fructofuranos
775	62.5	5.1	698	2	T12161	NADH2 dehydrogenas
776	62.5	5.1	700	2	T12162	NADH2 dehydrogenas
777	62.5	5.1	711	2	D86296	hypothetical prote
778	62.5	5.1	715	2	B83222	regulatory protein
779	62.5	5.1	718	2	A99195	hypothetical prote
780	62.5	5.1	849	2	T01286	probable RNA-bind
781	62.5	5.1	855	1	J02003	env polyprotein -
782	62.5	5.1	1021	2	A28199	Na+/K+-exchanging
783	62.5	5.1	1070	2	F90106	IAP100 protein lim
784	62.5	5.1	1079	2	I59362	calcium/polyvalent
785	62.5	5.1	1083	2	S76111	acridflavin resista
786	62.5	5.1	1242	2	G88480	protein C16A3.7 [i
787	62.5	5.1	1289	2	S69689	hypothetical prote
788	62.5	5.1	1523	2	T13953	MEGF5, protein - ra
789	62.5	5.1	1560	2	T00080	hypothetical prote
790	62.5	5.1	1811	2	T00035	nonstructural poly
791	62	5.1	165	2	AG1903	hypothetical prote
792	62	5.1	167	2	T15114	cytochrome-c oxida
793	62	5.1	261	2	G58888	acyl-CoA thioester
794	62	5.1	265	2	B97272	gamma-glutamyl hyd
795	62	5.1	318	2	JC6115	phosphate transpor
796	62	5.1	319	1	BVECPW	phosphate transpor
797	62	5.1	319	2	AC0956	phosphate transpor
798	62	5.1	319	2	G86057	phosphate transpor
799	62	5.1	319	2	G91211	phosphate transpor
800	62	5.1	320	2	S17177	probable G protein
801	62	5.1	324	1	C69861	toxic anion resist
802	62	5.1	335	2	T32657	hypothetical prote
803	62	5.1	358	2	I38429	connexin40 - human
804	62	5.1	365	2	F85018	hypothetical prote
805	62	5.1	365	2	H71268	conserved hypotnet
806	62	5.1	369	2	A72453	hypothetical prote
807	62	5.1	379	1	S17411	ubiquinol-cytochro
808	62	5.1	382	1	S33573	ubiquinol-cytochro
809	62	5.1	388	1	D70006	conserved hypotnet
810	62	5.1	402	2	B75297	dipeptidyl peptida
811	62	5.1	414	2	AI0156	probable tryptopha
812	62	5.1	421	2	T27311	hypothetical prote
813	62	5.1	427	2	F97790	hypothetical prote
814	62	5.1	429	2	AG3150	putrescine-ornithi
815	62	5.1	432	2	A84798	hypothetical prote
816	62	5.1	433	2	S77340	hypothetical prote
817	62	5.1	439	2	B40839	putrescine/ornithi
818	62	5.1	439	2	H90718	putrescine transpo
819	62	5.1	439	2	H85568	putrescine transpo
820	62	5.1	444	2	T32648	hypothetical prote
821	62	5.1	445	2	T05887	hypothetical prote
822	62	5.1	447	2	F75016	hypothetical prote
823	62	5.1	448	2	F95036	PTS system, IIC co
824	62	5.1	448	2	B97907	phosphotransferase
826	62	5.1	450	2	AI2324	glucan 1,3-beta-gl
827	62	5.1	452	2	C71391	NADH2 dehydrogenas
828	62	5.1	473	2	T04965	amino acid transpo
829	62	5.1	488	1	OXASM4	NADH2 dehydrogenas
830	62	5.1	492	2	E96731	endo-1,4-beta-gluc
831	62	5.1	520	2	H97274	uncharacterized me
832	62	5.1	598	2	T05130	hypothetical prote



833	62	5.1	609	2	T32456	hypothetical prote	906	61.5	5.1	647	2	UQ2149	B west mating prot
834	62	5.1	610	2	T11544	NADH2 dehydrogenas	907	61.5	5.1	651	2	F82124	cytochrome c-type
835	62	5.1	628	2	B91146	probable integral	908	61.5	5.1	661	2	S37591	beta-fructofuranos
836	62	5.1	628	2	F85991	hypothetical integral	909	61.5	5.1	661	2	S37590	beta-fructofuranos
837	62	5.1	631	2	B98137	hypothetical 46.1k	910	61.5	5.1	670	1	DNOBUS	NADH2 dehydrogenas
838	62	5.1	640	2	D70850	probable oxidoredu	911	61.5	5.1	673	2	S59263	probable membrane
839	62	5.1	646	2	JN0473	P-selectin precurs	912	61.5	5.1	677	1	A45264	system b(0,+) amin
840	62	5.1	659	2	AF3489	cytochrome o ubiqu	913	61.5	5.1	698	2	T12559	NADH2 dehydrogenas
841	62	5.1	662	2	T01857	hypothetical prote	914	61.5	5.1	699	2	T12167	NADH2 dehydrogenas
842	62	5.1	771	2	S45048	capsid protein - h	915	61.5	5.1	699	2	T12172	NADH2 dehydrogenas
843	62	5.1	826	2	T15751	hypothetical prote	916	61.5	5.1	787	2	S09411	DNA translocase sp
844	62	5.1	949	1	PXMUP1	H+-exporting ATPas	917	61.5	5.1	799	2	T48451	myotubularin-like
845	62	5.1	972	2	E97421	NADH dehydrogenase	918	61.5	5.1	889	2	JC6015	chitin synthase (E
846	62	5.1	994	2	AD2639	pH adaptin potass	919	61.5	5.1	898	2	D86122	Mg(2+) transport ATP
847	62	5.1	1083	2	T05689	hypothetical prote	920	61.5	5.1	898	2	B65236	Mg(2+) transport ATP
848	62	5.1	1166	2	T13958	synGAP-b1 protein	921	61.5	5.1	898	2	C91281	Mg2+ transport ATP
849	62	5.1	1249	2	T14270	Ras-GTPase activat	922	61.5	5.1	929	2	C90531	cation-transportin
850	62	5.1	1293	2	T14259	ras GTPase-activat	923	61.5	5.1	972	2	S67048	MTR10 protein - ye
851	62	5.1	2139	2	A44467	voltage-dependent	924	61.5	5.1	1029	2	AG3363	SMT4 protein - yea
852	62	5.1	3119	2	I49729	HD protein - mouse	925	61.5	5.1	1034	2	S43947	gene p2 protein -
853	61.5	5.1	115	2	A23329	Ly-5-8 glycoprotei	926	61.5	5.1	1344	2	S47412	E2 glycoprotein pr
854	61.5	5.1	161	2	I37034	eosinophil-derived	927	61.5	5.1	1449	2	S47423	probable ABC trans
855	61.5	5.1	222	2	T27916	hypothetical prote	928	61.5	5.1	1488	2	F86428	genome polyprotein
856	61.5	5.1	238	2	T23352	thiol-disulfide in	929	61.5	5.1	2179	1	GNNYH4	hypothetical prote
857	61.5	5.1	248	2	S76774	hypothetical prote	930	61	5.0	189	2	A71569	hypothetical prote
858	61.5	5.1	257	2	AC1290	hypothetical prote	931	61	5.0	193	2	B91170	hypothetical membr
859	61.5	5.1	260	2	I45938	MHC cell surface g	932	61	5.0	193	2	B86016	hypothetical prote
860	61.5	5.1	268	2	D29312	MHC class II histo	933	61	5.0	200	2	S43593	hypothetical prote
861	61.5	5.1	272	2	T09132	26S proteasome bet	934	61	5.0	213	2	A34633	M04D8.6 protein -
862	61.5	5.1	281	2	C69504	probable heme A fa	935	61	5.0	216	2	C87037	H+-exporting ATPas
863	61.5	5.1	301	1	S10456	cytochrome c-type	936	61	5.0	226	2	I49589	antigen - mouse
864	61.5	5.1	325	1	B40358	NADH2 dehydrogenas	937	61	5.0	226	2	T44070	conserved hypotHet
865	61.5	5.1	325	1	DNWTU1	NADH2 dehydrogenas	938	61	5.0	251	2	E64604	conserved hypotHet
866	61.5	5.1	325	1	S49576	NADH2 dehydrogenas	939	61	5.0	255	2	E64604	conserved hypotHet
867	61.5	5.1	325	2	T32282	hypothetical prote	940	61	5.0	257	2	I54285	MHC class II histo
868	61.5	5.1	336	2	S75437	hypothetical prote	941	61	5.0	274	2	C47700	glycerol uptake fa
869	61.5	5.1	335	2	S41686	geranylgeranyltran	942	61	5.0	282	2	T03906	cytochrome B561 ho
870	61.5	5.1	362	2	A39714	G protein-coupled	943	61	5.0	287	2	C82158	R0K family protein
871	61.5	5.1	371	1	A75033	probable hexosyltr	944	61	5.0	297	2	D83409	probable membrane
872	61.5	5.1	377	2	G90737	hypothetical prote	945	61	5.0	302	2	T03109	probable membrane
873	61.5	5.1	377	2	H85587	hypothetical prote	946	61	5.0	302	2	C64311	Na+/Ca2+-exchangin
874	61.5	5.1	377	2	A64816	ybbs protein - Esc	947	61	5.0	316	2	B83768	D-3-phosphoglycerat
875	61.5	5.1	385	2	I51307	basolateral Na(+)-	948	61	5.0	322	2	D96921	oligopeptide trans
876	61.5	5.1	391	2	AB1285	transmembrane tran	949	61	5.0	326	2	S70596	NADH2 dehydrogenas
877	61.5	5.1	394	2	S23481	benz protein - Aci	950	61	5.0	348	2	T04923	hypothetical prote
878	61.5	5.1	397	2	AF3285	membrane protein m	951	61	5.0	369	2	S74017	hypothetical prote
879	61.5	5.1	417	2	AG1934	folylpolyglutamete	952	61	5.0	375	2	C97217	hypothetical prote
880	61.5	5.1	444	2	D97142	surface-layer rela	953	61	5.0	379	1	S17417	gGDEF domain conta
881	61.5	5.1	461	2	T11819	glycerol-3-phospha	954	61	5.0	379	1	S41833	ubiquinol-cytochro
882	61.5	5.1	462	2	D26488	tubulin alpha-4 ch	955	61	5.0	379	2	I48135	ubiquinol-cytochro
883	61.5	5.1	468	2	T41294	hypothetical prote	956	61	5.0	379	2	T11401	ubiquinol-cytochro
884	61.5	5.1	472	2	E81784	glutamate-ammonia	957	61	5.0	380	2	T11803	ubiquinol-cytochro
885	61.5	5.1	481	2	T27435	hypothetical prote	958	61	5.0	382	2	S73256	hypothetical prote
886	61.5	5.1	487	2	T49424	hypothetical prote	959	61	5.0	392	2	E91290	probable transport
887	61.5	5.1	491	2	B86096	xylose-proton symp	960	61	5.0	392	2	H86131	probable transport
888	61.5	5.1	491	2	F91255	xylose-proton symp	961	61	5.0	401	2	H69833	conserved hypotHet
889	61.5	5.1	497	1	A26430	membrane protein p	962	61	5.0	402	2	G89911	conserved hypotHet
890	61.5	5.1	497	1	WMBELM	xylose transport L	963	61	5.0	412	2	S13035	aspartate transami
891	61.5	5.1	504	2	A83901	hypothetical prote	964	61	5.0	413	2	S29028	aspartate transami
892	61.5	5.1	510	1	DERZN2	NADH2 dehydrogenas	965	61	5.0	413	2	S29028	aspartate transami
893	61.5	5.1	510	2	S65075	NADH2 dehydrogenas	966	61	5.0	429	2	AH2409	hypothetical prote
894	61.5	5.1	512	2	E96024	conserved hypotHet	967	61	5.0	430	2	B83633	hypothetical prote
895	61.5	5.1	516	2	T47509	probable transport	968	61	5.0	445	2	AI2724	potassium uptake p
896	61.5	5.1	524	2	S28902	glutamate transpor	969	61	5.0	445	2	B83931	hypothetical prote
897	61.5	5.1	530	2	T04871	hypothetical prote	970	61	5.0	448	2	S40439	hypothetical prote
898	61.5	5.1	533	2	E64626	ABC transporter, A	971	61	5.0	460	1	S48489	tubulin alpha-2 ch
899	61.5	5.1	533	2	H71886	probable ABC trans	972	61	5.0	463	2	G85781	allantoinase (EC 3
900	61.5	5.1	537	2	T02982	probable sucrose t	973	61	5.0	463	2	C90933	part of a kinase f
901	61.5	5.1	538	2	E72752	hypothetical prote	974	61	5.0	466	2	S36577	L2 protein - human
902	61.5	5.1	543	2	S65462	glucose transport	975	61	5.0	467	2	S33181	glutamate-ammonia
903	61.5	5.1	547	2	D95337	probable manganese	976	61	5.0	475	2	T33943	hypothetical prote
904	61.5	5.1	575	2	D71642	glutathione-regula	977	61	5.0	480	2	S50525	hypothetical prote
905	61.5	5.1	611	2	T21747	hypothetical prote	978	61	5.0	485	2	B97506	potassium uptake p

979	61	5.0	494	2	S16068	testosterone 15alp
980	61	5.0	494	2	A32030	coumarin 7-monooxy
981	61	5.0	503	2	F71038	probable pyrimidin
982	61	5.0	532	2	H96840	hypothetical prote
983	61	5.0	535	2	T47629	phosphate transpor
984	61	5.0	545	2	S59143	NADH2 dehydrogenas
985	61	5.0	555	2	T38108	high-affinity gluc
986	61	5.0	574	2	AC1414	ABC transporter re
987	61	5.0	576	2	S14834	lysine-trRNA ligase
988	61	5.0	583	2	T32266	hypothetical prote
989	61	5.0	585	2	B49596	genome polypotein
990	61	5.0	598	2	S66954	probable membrane
991	61	5.0	602	2	T11438	NADH2 dehydrogenas
992	61	5.0	602	2	AB0024	probable potassium
993	61	5.0	610	2	T26761	hypothetical prote
994	61	5.0	648	2	T47988	serine/threonine-p
995	61	5.0	659	2	D72083	transport ATP bind
996	61	5.0	659	2	C86542	Transport ATP Bind
997	61	5.0	668	2	T05257	probable disease r
998	61	5.0	700	2	B69146	sensory transducti
999	61	5.0	715	2	AF1829	two-component hybr
1000	61	5.0	770	2	T23999	hypothetical prote
1001	61	5.0	970	2	A13605	potassium efflux s
1002	61	5.0	1036	2	A42895	H+/K+-exchanging A
1003	61	5.0	1037	2	S37879	nuclear pore prote
1004	61	5.0	1041	2	C87645	AcrB/AcrD/AcrF fam
1005	61	5.0	1043	2	T13172	gag-like protein p
1006	61	5.0	1065	2	H95321	NolG efflux transp
1007	61	5.0	1198	2	T49726	hypothetical prote
1008	61	5.0	1441	2	A88355	protein Y48B1A.1 f
1009	61	5.0	1545	1	S71841	multidrug resistan
1010	61	5.0	1737	2	T19606	hypothetical prote
1011	61	5.0	1821	2	AG2335	hypothetical prote
1012	61	5.0	1869	2	A59290	class V chitin syn
1013	61	5.0	2220	2	A45290	calcium channel pr
1014	61	5.0	2220	2	B71619	hypothetical prote
1015	61	5.0	2539	2	B71619	probable membrane
1016	60.5	5.0	119	2	B87205	Ig kappa chain V r
1017	60.5	5.0	151	2	S41816	probable integral
1018	60.5	5.0	165	2	B72727	hypothetical prote
1019	60.5	5.0	167	2	F84867	hypothetical prote
1020	60.5	5.0	212	2	T26887	hypothetical prote
1021	60.5	5.0	232	2	I47094	MHC class II OLA-D
1022	60.5	5.0	243	2	E70986	hypothetical prote
1023	60.5	5.0	264	2	A75076	membrane protein p
1024	60.5	5.0	267	2	E89870	hypothetical prote
1025	60.5	5.0	269	2	S65034	cytochrome-c oxida
1026	60.5	5.0	276	2	E65072	hypothetical prote
1027	60.5	5.0	277	2	D98085	hypothetical prote
1028	60.5	5.0	278	2	E95221	sugar ABC transpor
1029	60.5	5.0	283	2	T22776	hypothetical prote
1030	60.5	5.0	283	2	AE2081	hypothetical prote
1031	60.5	5.0	289	2	B43747	hypothetical prote
1032	60.5	5.0	289	2	B43748	hypothetical prote
1033	60.5	5.0	293	1	QOCVPY	BLI protein - pota
1034	60.5	5.0	300	2	S15786	glucose transport
1035	60.5	5.0	304	2	A97768	probable protease
1036	60.5	5.0	305	2	C89915	hypothetical prote
1037	60.5	5.0	314	2	T21003	hypothetical prote
1038	60.5	5.0	315	2	D64458	branched-chain ami
1039	60.5	5.0	323	2	T15808	hypothetical prote
1040	60.5	5.0	328	2	D45774	odorant receptor 3
1041	60.5	5.0	332	2	AE2438	thiamin monophosph
1042	60.5	5.0	344	2	T04924	hypothetical prote
1043	60.5	5.0	349	2	S59648	hypothetical prote
1044	60.5	5.0	363	2	T24809	hypothetical prote
1045	60.5	5.0	363	2	S42386	hypothetical prote
1046	60.5	5.0	379	1	S17414	ubiquinol-cytochro
1047	60.5	5.0	379	2	S58462	ubiquinol-cytochro
1048	60.5	5.0	382	1	A39802	gap junction prote
1049	60.5	5.0	382	1	S00532	gap junction prote
1050	60.5	5.0	383	1	A36623	gap junction prote
1051	60.5	5.0	384	2	A86521	hypothetical prote
		1052				hypothetical prote
		1053				unknown protein F1
		1054				probable transport
		1055				MFS fermease [limpo
		1056				probable MFS trans
		1057				probable pectinase
		1058				NADH2 dehydrogenas
		1059				probable integral
		1060				dicarboxylic acid
		1061				hypothetical prote
		1062				nickel resistance
		1063				NADH2 dehydrogenas
		1064				probable V-type AT
		1065				hypothetical prote
		1066				hypothetical prote
		1067				aminic acid permeas
		1068				ubiquinone oxidore
		1069				probable sodium-tr
		1070				multidrug resistan
		1071				BIO3 protein - yea
		1072				Cytochrome-c oxida
		1073				MFS fermease [limpo
		1074				testosterone 7alpn
		1075				NADH2 dehydrogenas
		1076				hypothetical prote
		1077				hypothetical prote
		1078				hypothetical prote
		1079				hypothetical prote
		1080				2-amino-4-hydroxy-
		1081				sucrose synthase (
		1082				NADH2 dehydrogenas
		1083				lipopolysaccharide
		1084				lactase permease -
		1085				cytochrome c-type
		1086				sodium/phosphate c
		1087				probable sulfate t
		1088				type I transmembra
		1089				hypothetical prote
		1090				NADH2 dehydrogenas
		1091				NADH2 dehydrogenas
		1092				NADH2 dehydrogenas
		1093				NADH2 dehydrogenas
		1094				NADH2 dehydrogenas
		1095				NADH2 dehydrogenas
		1096				probable lysophosp
		1097				hypothetical prote
		1098				hypothetical prote
		1099				hypothetical prote
		1100				hypothetical prote
		1101				hypothetical prote
		1102				sucrose syntnase (
		1103				hypothetical prote
		1104				hypothetical prote
		1105				cation-transportin
		1106				hypothetical prote
		1107				hypothetical prote
		1108				probable P-glycopr
		1109				probable DNA gyras
		1110				DNA topoisomerase
		1111				E2 g-glycoprotein pr
		1112				E2 g-glycoprotein -
		1113				T16G.2.5 protein -
		1114				hypothetical prote
		1115				cell division prot
		1116				G surface protein
		1117				hypothetical prote
		1118				BIR repeat contain
		1119				hypothetical prote
		1120				disulfide bond oxi
		1121				disulfide bond oxi
		1122				hypothetical prote
		1123				22K antigen - Rick
		1124				hypothetical prote
		1124				nolH protein - Rhi

1125	60	4.9	228	1	A40402	CD9 antigen [valid
1126	60	4.9	228	1	A42929	CD9 antigen - gree
1127	60	4.9	228	2	B90369	hypothetical prote
1128	60	4.9	234	2	AG1220	glycerol uptake fa
1129	60	4.9	251	2	H69441	carboxylesterase (
1130	60	4.9	257	2	A11661	hypothetical prote
1131	60	4.9	258	2	I54458	MHC class II histo
1132	60	4.9	265	2	A83969	hypothetical prote
1133	60	4.9	268	2	T24795	hypothetical prote
1134	60	4.9	287	2	T18735	hypothetical prote
1135	60	4.9	291	2	E91089	prolipoprotein dia
1136	60	4.9	291	2	G85934	prolipoprotein dia
1137	60	4.9	291	2	A56149	prolipoprotein dia
1138	60	4.9	293	2	AF2904	ABC transporter, m
1139	60	4.9	293	2	H97679	probable ABC trans
1140	60	4.9	301	2	S76574	hypothetical prote
1141	60	4.9	303	2	AE3129	conserved hypothet
1142	60	4.9	303	2	D98158	hypothetical prote
1143	60	4.9	307	2	G84962	hypothetical prote
1144	60	4.9	309	2	T40759	synthaxin, vesicula
1145	60	4.9	338	2	G70584	phosphate transpor
1146	60	4.9	348	2	E86818	dehydrogenase (imp
1147	60	4.9	350	2	B82281	ferric vibriobacti
1148	60	4.9	355	2	I51319	RH2 opsin - green
1149	60	4.9	357	2	T33237	hypothetical prote
1150	60	4.9	365	2	I38748	prostaglandin recep
1151	60	4.9	365	2	S51315	prostaglandin E re
1152	60	4.9	370	2	H90559	hypothetical prote
1153	60	4.9	374	2	I38747	prostaglandin recep
1154	60	4.9	374	2	S51317	prostaglandin E re
1155	60	4.9	374	2	T26200	hypothetical prote
1156	60	4.9	379	1	S41834	ubiquinol-cytochro
1157	60	4.9	379	1	S43267	ubiquinol-cytochro
1158	60	4.9	379	2	S58450	ubiquinol-cytochro
1159	60	4.9	379	2	AE3225	ABC transporter, m
1160	60	4.9	380	2	JI0053	UDPglucose-hexose-
1161	60	4.9	380	2	E81302	probable type I re
1162	60	4.9	381	2	T11440	ubiquinol-cytochro
1163	60	4.9	381	2	T23250	hypothetical prote
1164	60	4.9	382	2	G90751	probable transport
1165	60	4.9	382	2	E85615	probable transpor
1166	60	4.9	382	2	A64829	membrane protein Y
1167	60	4.9	388	2	S51316	prostaglandin E re
1168	60	4.9	388	2	I38750	prostaglandin recep
1169	60	4.9	390	2	S43375	prostaglandin E re
1170	60	4.9	390	2	S51313	prostaglandin E re
1171	60	4.9	393	2	AC2782	diaminopimelate de
1172	60	4.9	393	2	S51318	prostaglandin E re
1173	60	4.9	393	2	E96954	Na/H antiporter (n
1174	60	4.9	394	2	AE1196	D1cB protein for D
1175	60	4.9	400	2	AG0068	cell division prot
1176	60	4.9	403	2	G64427	hypothetical prote
1177	60	4.9	405	2	AE1474	probable permease
1178	60	4.9	412	2	S72579	hypothetical prote
1179	60	4.9	417	2	A45794	tubulin alpha chai
1180	60	4.9	422	2	AB3635	probable O-antigen
1181	60	4.9	425	2	S51319	prostaglandin E re
1182	60	4.9	436	2	AC1021	proton glutamate s
1183	60	4.9	437	2	JC5459	inulin fructotrans
1184	60	4.9	440	2	D97561	btcrk (AB033991) [i
1185	60	4.9	449	2	C75053	DNA damage-inducib
1186	60	4.9	452	2	F64730	UDP-N-acetylmuramo
1187	60	4.9	455	2	T37517	hypothetical prote
1188	60	4.9	458	2	B81409	probable transmemb
1189	60	4.9	462	2	D81251	NADH2 dehydrogenas
1190	60	4.9	463	2	S59968	secY protein - Sul
1191	60	4.9	465	2	H87627	response regulator
1192	60	4.9	469	2	AE3374	glutamate-ammonia
1193	60	4.9	474	2	T34193	G protein-coupled
1194	60	4.9	476	2	H82085	sodium/alanine sym
1195	60	4.9	478	2	A37430	calcitonin recepto
1196	60	4.9	479	2	S33746	calcitonin recepto
1197	60	4.9	491	2	G84498	hypothetical prote
1198	60	4.9	502	2	E87596	tryptophan halogen
1199	60	4.9	508	2	T19350	hypothetical prote
1200	60	4.9	509	2	A32101	glucose transport
1201	60	4.9	534	2	C84811	phosphate transpor
1202	60	4.9	556	2	H82287	malate synthase A
1203	60	4.9	557	2	AE0204	methyl-accepting c
1204	60	4.9	557	2	T46520	probable transmemb
1205	60	4.9	557	2	S58688	hypothetical prote
1206	60	4.9	577	2	T32336	hypothetical prote
1207	60	4.9	578	2	T35537	cytochrome-c oxida
1208	60	4.9	603	2	H69121	hypothetical prote
1209	60	4.9	608	2	T25572	hypothetical prote
1210	60	4.9	616	2	A30304	prolactin receptor
1211	60	4.9	623	2	C86184	hypothetical prote
1212	60	4.9	633	2	S45877	uracil transport p
1213	60	4.9	635	2	S30018	allantoin transpor
1214	60	4.9	638	2	T11801	NADH2 dehydrogenas
1215	60	4.9	640	2	S23008	insulin-like growt
1216	60	4.9	679	2	A83488	hypothetical prote
1217	60	4.9	703	2	T13074	NADH2 dehydrogenas
1218	60	4.9	746	1	HYHUMA	meprin A (EC 3.4.2
1219	60	4.9	795	2	T31180	hypothetical prote
1220	60	4.9	795	2	H70934	hypothetical prote
1221	60	4.9	860	2	T49910	hypothetical prote
1222	60	4.9	933	2	C83514	probable NADH dehy
1223	60	4.9	960	2	T06688	H+-exporting ATPas
1224	60	4.9	975	2	T16073	hypothetical prote
1225	60	4.9	1033	2	T49179	Ca2+-transporting
1226	60	4.9	1095	2	A54145	sodium-potassium-c
1227	60	4.9	1128	2	T04922	hypothetical prote
1228	60	4.9	1307	2	T25106	hypothetical prote
1229	60	4.9	1402	2	T24664	hypothetical prote
1230	60	4.9	1487	2	G96827	protein F20B17.10
1231	60	4.9	1492	2	T18560	DNA-directed DNA p
1232	60	4.9	1592	2	S48933	probable transport
1233	60	4.9	1945	2	T13937	plexin A - fruit f
1234	60	4.9	2090	2	T30075	hypothetical prote
1235	60	4.9	2153	2	T30074	hypothetical prote
1236	60	4.9	2201	2	AH0095	probable sideropho
1237	60	4.9	2476	2	T34022	zonadhesin - pig
1238	60	4.9	3144	2	A46068	Huntington disease
1239	59.5	4.9	88	2	G82754	hypothetical prote
1240	59.5	4.9	92	2	D43674	US5 protein - huma
1241	59.5	4.9	112	2	A46717	collipase precursor
1242	59.5	4.9	128	2	S40379	ig kappa chain V-J
1243	59.5	4.9	150	2	C86876	hypothetical prote
1244	59.5	4.9	155	2	D72761	hypothetical prote
1245	59.5	4.9	161	2	A33922	eosinophil-derived
1246	59.5	4.9	198	1	A60620	prolactin - green
1247	59.5	4.9	204	2	AI0059	probable Lyse type
1248	59.5	4.9	227	2	H90109	27.2K hypothetical
1249	59.5	4.9	234	2	AB1574	glycerol uptake fa
1250	59.5	4.9	234	2	T30473	late expression fa
1251	59.5	4.9	235	2	AD2904	RhbB family transp
1252	59.5	4.9	235	2	F97679	hypothetical prote
1253	59.5	4.9	239	2	G64810	pncC protein - Bsc
1254	59.5	4.9	242	2	A69026	conserved hypothet
1255	59.5	4.9	244	2	B83142	hypothetical prote
1256	59.5	4.9	255	2	D71910	hypothetical prote
1257	59.5	4.9	261	2	S68134	cytochrome-c oxida
1258	59.5	4.9	263	2	S72528	chitinase (EC 3.2.
1259	59.5	4.9	270	2	AF2008	permease protein o
1260	59.5	4.9	287	2	A25877	cytochrome-c oxida
1261	59.5	4.9	289	2	H86880	transporter yvvd I
1262	59.5	4.9	291	2	S73242	hypothetical prote
1263	59.5	4.9	293	1	QOBEG1	HVUF1 protein - hu
1264	59.5	4.9	307	2	B82394	hypothetical prote
1265	59.5	4.9	309	2	T31908	hypothetical prote
1266	59.5	4.9	310	2	S64619	probable membrane
1267	59.5	4.9	318	2	AB0350	probable membrane
1268	59.5	4.9	321	2	T45986	hypothetical prote
1269	59.5	4.9	324	2	H86533	integral membrane
1270	59.5	4.9	324	2	H72088	ABC transporter, p

1271	59.5	4.9	327	2	G88976	protein F54E2.6 [i	1344	59.5	4.9	615	2	H82635	hypothetical prote
1272	59.5	4.9	328	2	T11938	NADH2 dehydrogenas	1345	59.5	4.9	622	2	B71326	probable V-type AT
1273	59.5	4.9	329	2	H83907	cytochrome a3 qui	1346	59.5	4.9	626	2	H82133	conserved hypothet
1274	59.5	4.9	336	2	AC2413	hypothetical prote	1347	59.5	4.9	633	2	T33306	hypothetical prote
1275	59.5	4.9	337	2	A53041	effector cell prot	1348	59.5	4.9	646	2	T48902	sulfate transporte
1276	59.5	4.9	341	2	F82301	peptide ABC transp	1349	59.5	4.9	658	2	T49069	sulfate transporte
1277	59.5	4.9	343	2	D83282	probable peymease	1350	59.5	4.9	658	2	T48901	sulfate transporte
1278	59.5	4.9	343	2	G89795	hypothetical prote	1351	59.5	4.9	660	2	H87590	cytochrome c-type
1279	59.5	4.9	345	2	AD2998	transporter Atu359	1352	59.5	4.9	682	2	T18847	hypothetical prote
1280	59.5	4.9	345	2	E98285	yFkh (AJO10131) [i	1353	59.5	4.9	686	2	A45483	chloride channel,
1281	59.5	4.9	353	1	D65025	probable peymease	1354	59.5	4.9	699	2	T12170	NADH2 dehydrogenas
1282	59.5	4.9	353	2	G85892	probable peymease	1355	59.5	4.9	699	2	T12173	hypothetical prote
1283	59.5	4.9	353	2	C91048	probable peymease	1356	59.5	4.9	703	2	T51161	hypothetical prote
1284	59.5	4.9	355	2	T32723	hypothetical prote	1357	59.5	4.9	710	2	S62575	hypothetical prote
1285	59.5	4.9	366	2	T50468	probable maturase	1358	59.5	4.9	714	2	S76082	hypothetical prote
1286	59.5	4.9	376	2	A86382	43.4K hypothetical	1359	59.5	4.9	726	2	S22258	probable protein k
1287	59.5	4.9	379	1	S41847	ubiquinol-cytochro	1360	59.5	4.9	778	2	T05341	S-receptor kinase
1288	59.5	4.9	379	2	S58454	ubiquinol-cytochro	1361	59.5	4.9	800	2	G89831	hypothetical prote
1289	59.5	4.9	379	2	H82284	queuine tRNA-ribos	1362	59.5	4.9	821	2	T41364	hypothetical prote
1290	59.5	4.9	387	2	T31748	hypothetical prote	1363	59.5	4.9	828	2	E71417	hypothetical prote
1291	59.5	4.9	396	2	S01660	glycerol-3-phospha	1364	59.5	4.9	914	1	JN0550	iodide peroxidase
1292	59.5	4.9	396	2	T39337	hypothetical prote	1365	59.5	4.9	953	2	S19427	probable membrane
1293	59.5	4.9	402	2	AG0638	probable membrane	1366	59.5	4.9	1027	2	T43024	ceoB protein - Bur
1294	59.5	4.9	410	2	E75048	multidrug resistan	1367	59.5	4.9	1088	2	T41671	hypothetical prote
1295	59.5	4.9	410	2	D71897	hypothetical prote	1368	59.5	4.9	1129	2	D84022	ATP-cèpendent nucl
1296	59.5	4.9	418	2	G70864	probable transmemb	1369	59.5	4.9	1161	2	B70172	DNA polymerase III
1297	59.5	4.9	428	2	T25950	hypothetical prote	1370	59.5	4.9	1187	2	T20544	hypothetical prote
1298	59.5	4.9	430	2	T12541	hypothetical prote	1371	59.5	4.9	1217	2	T13996	pol protein - frui
1299	59.5	4.9	431	1	SAVLC2	large surface anti	1372	59.5	4.9	1220	2	T18291	patched protein -
1300	59.5	4.9	433	2	T17654	hypothetical prote	1373	59.5	4.9	1237	2	A54080	protein-tyrosine-p
1301	59.5	4.9	433	2	T27731	hypothetical prote	1374	59.5	4.9	1247	2	T18671	hypothetical prote
1302	59.5	4.9	437	2	A36372	membrane transport	1375	59.5	4.9	1268	2	G85154	hypothetical prote
1303	59.5	4.9	440	2	T11319	NADH2 dehydrogenas	1376	59.5	4.9	1289	1	GUBPT4	proximal tail fibe
1304	59.5	4.9	441	2	S47049	1-aminocyclopropan	1377	59.5	4.9	1429	2	T19422	hypothetical prote
1305	59.5	4.9	445	2	T42366	L-aminoadipate-sem	1378	59.5	4.9	1584	2	T18276	protein-tyrosine k
1306	59.5	4.9	449	2	A48466	tubulin alpha chai	1379	59.5	4.9	1758	2	F88559	protein C48B4.4b [
1307	59.5	4.9	457	2	T15271	hypothetical prote	1380	59.5	4.9	1807	2	JC6319	integrin beta-4 ch
1308	59.5	4.9	465	2	S03325	transforming prote	1381	59.5	4.9	1964	2	T09059	notch4 - mouse
1309	59.5	4.9	466	2	T41125	glucose-triggered	1382	59.5	4.9	2514	2	T37320	ataxia telangiecta
1310	59.5	4.9	469	2	AC3584	methylenomycin a r	1383	59.5	4.9	2619	2	T24588	hypothetical prote
1311	59.5	4.9	476	2	H96802	probable amino aci	1384	59.5	4.9	3766	2	T29165	hypothetical prote
1312	59.5	4.9	479	2	T47415	transporter-like p	1385	59.5	4.9	3944	2	T19997	hypothetical prote
1313	59.5	4.9	483	2	H97246	UDP-N-acetylmuramy	1386	59	4.9	125	2	T49512	hypothetical prote
1314	59.5	4.9	483	2	I55598	diabetes-associate	1387	59	4.9	158	2	A11184	hypothetical prote
1315	59.5	4.9	485	1	KIBYHA	hexokinase (EC 2.7	1388	59	4.9	208	2	T05859	hypothetical prote
1316	59.5	4.9	499	1	S30007	proline rich prote	1389	59	4.9	208	2	A89773	hypothetical prote
1317	59.5	4.9	499	1	S30007	probable UTP-gluc	1390	59	4.9	219	2	D90448	hypothetical prote
1318	59.5	4.9	514	2	E86738	probable integral	1391	59	4.9	226	2	S57521	conserved hypothet
1319	59.5	4.9	514	2	E86738	multidrug resistan	1392	59	4.9	242	2	S60143	probable arsenical
1320	59.5	4.9	520	1	A42209	D-stereospecific a	1393	59	4.9	248	2	T01080	hypothetical prote
1321	59.5	4.9	520	2	T20007	hypothetical prote	1394	59	4.9	249	2	T25643	hypothetical prote
1322	59.5	4.9	525	2	T24647	hypothetical prote	1395	59	4.9	250	2	B64417	hypothetical prote
1323	59.5	4.9	530	2	AG3622	rtn protein [impor	1396	59	4.9	254	2	B90421	hypothetical prote
1324	59.5	4.9	535	2	G95155	hypothetical prote	1397	59	4.9	258	2	I596621	HDA-DPB1 - human
1325	59.5	4.9	535	2	B98022	hypothetical prote	1398	59	4.9	265	2	H90868	probable pump prot
1326	59.5	4.9	541	2	T31554	conserved hypothet	1399	59	4.9	265	2	A85750	hypothetical prote
1327	59.5	4.9	541	2	D97930	hypothetical prote	1400	59	4.9	277	2	AE1831	sn-glycerol-3-phos
1328	59.5	4.9	546	2	T23920	oligopeptide trans	1401	59	4.9	281	2	A10461	zinc finger protei
1329	59.5	4.9	552	2	T51439	hypothetical prote	1402	59	4.9	284	2	T06129	hypothetical prote
1330	59.5	4.9	557	1	S76051	hypothetical prote	1403	59	4.9	289	2	G83029	l1cB protein limpo
1331	59.5	4.9	567	2	H87370	major facillitator	1404	59	4.9	292	2	C95147	hypot:hetical prote
1332	59.5	4.9	567	2	A33974	membrane transport	1405	59	4.9	296	2	A98015	hypot:hetical limpo
1333	59.5	4.9	574	2	T14162	hABC transport pro	1406	59	4.9	305	2	E83890	sugar: transport sy
1334	59.5	4.9	576	2	T41407	membrane transport	1407	59	4.9	307	2	H71160	hypot:hetical prote
1335	59.5	4.9	577	1	G46328	hemagglutinin-neur	1408	59	4.9	310	2	A29884	prolactin receptor
1336	59.5	4.9	577	1	D46328	hemagglutinin-neur	1409	59	4.9	311	2	T32776	hypot:hetical prote
1337	59.5	4.9	577	1	HNNZNC	hemagglutinin-neur	1410	59	4.9	313	2	S06214	NADH?: dehydrogenas
1338	59.5	4.9	577	1	H81355	probable integral	1411	59	4.9	322	2	H96994	coba..amin bioynlth
1339	59.5	4.9	586	2	A95167	ABC transporter, A	1412	59	4.9	325	2	AH0796	NADH?: dehydrogenas
1340	59.5	4.9	601	2	T48539	probable potassium	1413	59	4.9	326	2	S59101	NADH?: dehydrogenas
1341	59.5	4.9	605	2	T11111	NADH2 dehydrogenas	1414	59	4.9	329	2	AC1718	ferr:chrome ABC tr
1342	59.5	4.9	607	1	QXMS5M	NADH2 dehydrogenas	1415	59	4.9	336	2	AF1378	B. subtilis ferric
1343	59.5	4.9	612	2	A97935	hypothetical prote	1416	59	4.9	336	2	AG1747	B. subtilis ferric

1417	59	4.9	343	2	A43577	regulatory protein
1418	59	4.9	345	2	C45456	NADH2 dehydrogenas
1419	59	4.9	346	2	T46914	hypothetical prote
1420	59	4.9	346	2	S49959	probable membrane
1421	59	4.9	348	1	COBO	rhodopsin - bovine
1422	59	4.9	349	2	AG3010	hypothetical prote
1423	59	4.9	349	2	G98273	iron(III) dicitrat
1424	59	4.9	353	2	S14203	NADH2 dehydrogenas
1425	59	4.9	353	2	C72479	hypothetical prote
1426	59	4.9	356	2	AE2729	cytochrome oxidase
1427	59	4.9	360	2	DB4646	hypothetical prote
1428	59	4.9	361	2	T34159	hypothetical prote
1429	59	4.9	363	2	B86229	hypothetical prote
1430	59	4.9	366	2	G95376	conserved hypothet
1431	59	4.9	372	2	F97510	BA483f11.2.1 (cox1
1432	59	4.9	378	2	T15816	hypothetical prote
1433	59	4.9	379	2	T11453	ubiquinol-cytochro
1434	59	4.9	379	2	T11869	ubiquinol-cytochro
1435	59	4.9	382	2	D58930	ubiquinol-cytochro
1436	59	4.9	385	2	G72638	hypothetical prote
1437	59	4.9	386	2	A26017	hypothetical prote
1438	59	4.9	387	2	E83679	patatin T5 precurs
1439	59	4.9	388	2	AC2011	multidrug-efflux t
1440	59	4.9	394	2	AB3073	hypothetical prote
1441	59	4.9	394	2	G98213	tetracycline resis
1442	59	4.9	395	2	E90896	drug efflux protei
1443	59	4.9	395	2	B85721	probable transport
1444	59	4.9	395	2	E90047	hypothetical prote
1445	59	4.9	401	2	S42583	phosphate transloc
1446	59	4.9	403	2	F83092	probable cytochrom
1447	59	4.9	404	2	S03638	triose phosphate/3
1448	59	4.9	408	2	G69819	Na+/H+ antiporter
1449	59	4.9	412	2	A26341	aspartate transami
1450	59	4.9	412	2	T34138	hypothetical prote
1451	59	4.9	412	2	A41070	prolactin receptor
1452	59	4.9	414	2	D82487	multidrug resistan
1453	59	4.9	414	2	S39530	poly(3-hydroxybuty
1454	59	4.9	415	2	D96759	probable serine ca
1455	59	4.9	415	2	E71848	probable nucleosid
1456	59	4.9	418	2	B69819	conserved hypothet
1457	59	4.9	420	2	F69144	O-antigen transpor
1458	59	4.9	428	2	AE1611	probable proteinas
1459	59	4.9	432	2	C85087	hypothetical prote
1460	59	4.9	433	2	S31436	Ig upsilon chain -
1461	59	4.9	433	2	B84566	hypothetical prote
1462	59	4.9	437	2	S11497	branched-chain ami
1463	59	4.9	438	2	AF3215	ABC transporter, m
1464	59	4.9	444	2	T27866	hypothetical prote
1465	59	4.9	444	2	C75428	probable permease
1466	59	4.9	445	2	C69596	branched-chain ami
1467	59	4.9	448	2	T22194	hypothetical prote
1468	59	4.9	449	2	S55911	tubulin alpha-1 ch
1469	59	4.9	449	2	T21415	hypothetical prote
1470	59	4.9	457	2	T12339	NADH2 dehydrogenas
1471	59	4.9	457	2	S18239	glycerol-3-phospha
1472	59	4.9	457	2	H64136	neurotransmitter t
1473	59	4.9	458	2	H82200	sodium/alanine sym
1474	59	4.9	461	2	T00621	hypothetical prote
1475	59	4.9	464	2	H83271	soluble pyridine n
1476	59	4.9	470	2	AB1804	transmembrane effl
1477	59	4.9	471	2	D64974	hypothetical prote
1478	59	4.9	471	2	H85834	probable transport
1479	59	4.9	471	2	E90989	probable transport
1480	59	4.9	473	2	T44709	acetyl/propionyl C
1481	59	4.9	476	2	A44170	membrane-bound rib
1482	59	4.9	487	1	QOECRS	ysjE protein - Bsc
1483	59	4.9	487	2	T19237	hypothetical prote
1484	59	4.9	493	2	I39541	cytolytic enteroto
1485	59	4.9	507	2	H75175	thymidine phosphor
1486	59	4.9	508	2	E90594	amino acid permeas
1487	59	4.9	517	2	S77255	glutamate prote
1488	59	4.9	523	2	S56777	glutamate transpor
1489	59	4.9	529	2	AF3059	cytochrome d oxida

1490	59	4.9	529	2	B98227	cytochrome d oxid
1491	59	4.9	534	1	S75101	hypothetical prote
1492	59	4.9	551	2	B64005	hypothetical prote
1493	59	4.9	552	2	B90476	hypothetical prote
1494	59	4.9	562	2	C71604	RNA helicase PFB08
1495	59	4.9	564	2	S73405	hexosephosphate tr
1496	59	4.9	581	2	B90539	hypothetical prote
1497	59	4.9	597	2	T23961	hypothetical prote
1498	59	4.9	598	2	T28238	ORF MSV077 hypothe
1499	59	4.9	603	2	S53301	H+-exporting ATPase
1500	59	4.9	610	2	A34631	lactogen receptor

## ALIGNMENTS

RESULT 1  
A42926  
L6 surface protein - human  
C/Species: Homo sapiens (man)  
C/Date: 01-Oct-1992 #sequence\_revision 01-Oct-1992 #text\_change 09-Jul-2004  
C/Accession: A42926  
R/Marken, J.S.; Schieven, G.L.; Hellstroem, I.; Hellstroem, K.E.; Aruffo, A.  
Proc. Natl. Acad. Sci. U.S.A. 89, 3503-3507, 1992  
A/Title: Cloning and expression of the tumor-associated antigen L6.  
A/Reference number: A42926; MUID:92228814; PMID:1565644  
A/Accession: A42926  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-202 <MAR>  
A/Cross-references: UNIPROT:P30408; GB:M90657; NID:g186803; PIDN:AAA36158.1; PID:g186803  
C/Keywords: transmembrane protein

### Query Match

Best Local Similarity 27.4%; Pred. No. 3.9e-08;  
Matches 62; Conservative 29; Mismatches 77; Indels 58; Gaps 8;

QY 10 CNGFSLVLLLGVLNATPLIVSLVEEDQFSQNPISCFEWMFPGLIGAG-LMAIPATTM 68  
| | : | | : | | : | | : | | : | | : | | :  
Db 9 CIHSLVGLALLCIAAN-ILLYFPNGETKYASENHLSRWVPFGSIGVGGLMLLPAYVF 67

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QY      69 SLARKRAC-----CNRRTGMFLSFFSVITVIGALYCMILISIQALLKGPLMCNPSN 12
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QY      122 SNANCEFLKNISDIHPESFNLQWFNFNSCAPPTGFNFKTSNDTMA5GWRASSFHPDSE- 18
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Db      127 -----QW-----NYTFA5--TEGQYLLDTST 14

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QY      181  -----ENKRL- IHFSVLGLLLVGIPEVLFGLSQIVIGFGCLG 220
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Db      146  WSECTEPKHIVEMNVSLFSLILALGIGIEFICLIQVINGVLGIGC 191
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## RESULT 2

JC6544

tumor-associated antigen TM4SF5 - human

C;Species: Homo sapiens (man)

C:\Date: 05-Dec-1998 #sequence\_ revision 05-Dec-1998 #text\_change 09-Jul-2004

C/Accession: J06544  
R;Mueller-Pillasch, F.; Wallrapp, C.; Lacher, U.; Friess, H.; Buechler, M.; Adler, G.; G  
Gene 208, 25-30, 1998

A;Title: Identification of a new tumour-associated anti  
A;Reference number: JC6544; MUID:98148000; PMID:94790388

**A;Accession:** JC6544

A;molecule type: mRNA

A;Residues: 1-197 <MUE>

A;Cross-references: UNIPROT:014894

**C;Comment:**

C;Genetics:

A;Gene: tm48f5

A;Map position: 17p13.3











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GenCore version 5.1.6  
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OM protein - protein search, using sw model1

Run on: January 24, 2005, 15:42:16 ; Search time 148 Seconds  
(without alignments)  
559.022 Million cell updates/sec

Perfect score: 1215  
Sequence: 1 MTCCEGWTSCNGFSLLVLL.....IVIGFLGCLCGVSKRSQIV 229

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
27	1215	100.0	229	10	US-09-997-428-258 Sequence 258, App
562	1215	100.0	229	14	US-10-174-587-198 Sequence 198, Appl
626	1215	100.0	229	14	US-10-063-742-48 Sequence 48, Appl
718	1215	100.0	229	14	US-10-063-550-48 Sequence 48, Appl
742	1209	99.5	229	13	US-10-087-192-66 Sequence 66, Appl
743	1205	99.2	229	16	US-10-755-889-508 Sequence 508, App
744	1189	97.9	227	17	US-10-331-053-36 Sequence 36, Appl
745	924.5	76.1	230	13	US-10-087-192-63 Sequence 63, Appl
746	907.5	74.7	228	17	US-10-331-053-33 Sequence 33, Appl
747	173.5	14.3	205	15	US-10-264-049-2362 Sequence 2362, Ap
748	170	14.0	197	11	US-09-973-278-154 Sequence 154, App
749	170	14.0	197	14	US-10-156-136-27 Sequence 27, Appl
750	170	14.0	198	10	US-09-983-802-232 Sequence 232, App
751	170	14.0	198	10	US-09-984-490-232 Sequence 232, App

752	170	14.0	202	10	US-09-284-320-84	Sequence 84, Appl
753	170	14.0	202	14	US-10-060-036-168	Sequence 168, App
754	170	14.0	202	14	US-10-156-136-41	Sequence 41, Appl
755	170	14.0	202	14	US-10-334-038-4	Sequence 4, Appli
756	170	14.0	202	14	US-10-295-027-1324	Sequence 1324, Ap
757	170	14.0	202	17	US-10-783-528-94	Sequence 94, Appl
758	166.5	13.7	202	14	US-10-060-036-4558	Sequence 4558, Ap
759	166.5	13.7	202	14	US-10-295-027-1303	Sequence 1303, Ap
760	166.5	13.7	202	17	US-10-783-528-84	Sequence 84, Appl
761	166	13.7	197	14	US-10-156-136-40	Sequence 40, Appl
762	144	11.9	153	9	US-09-925-301-1532	Sequence 1532, Ap
763	142	11.7	245	9	US-09-925-297-475	Sequence 475, App
764	140.5	11.6	145	10	US-09-866-050A-723	Sequence 723, App
765	126	10.4	201	14	US-10-156-136-28	Sequence 28, Appl
766	126	10.4	201	14	US-10-295-027-10	Sequence 10, Appl
767	126	10.4	201	15	US-10-211-462-12	Sequence 12, Appl
768	111.5	9.2	209	10	US-09-284-320-7	Sequence 7, Appli
769	88	7.2	1036	15	US-10-282-122A-76970	Sequence 76970, A
770	87.5	7.2	117	14	US-10-104-047-3823	Sequence 3823, Ap
771	87	7.2	1174	15	US-10-389-566-742	Sequence 742, App
772	87	7.2	1635	16	US-10-437-963-128533	Sequence 128533, A
773	86.5	7.1	891	15	US-10-174-587-84	Sequence 77590, A
774	86	7.1	449	10	US-09-882-227-406	Sequence 406, App
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776	85.5	7.0	356	15	US-10-144-929-114	Sequence 114, App
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1373	85.5	7.0	457	11	US-09-972-211-118	Sequence 118, App
1374	85.5	7.0	457	15	US-10-096-625-118	Sequence 118, App
1375	85.5	7.0	472	11	US-09-972-211-120	Sequence 120, App
1376	85.5	7.0	472	14	US-10-153-668-208	Sequence 208, App
1377	85.5	7.0	472	15	US-10-096-625-120	Sequence 120, App
1378	84	6.9	449	15	US-10-335-977-5387	Sequence 5387, Ap
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1380	82.5	6.8	185	10	US-09-925-302-718	Sequence 718, App
1381	82.5	6.8	261	11	US-09-833-245-1828	Sequence 1828, Ap
1382	82.5	6.8	1650	16	US-10-437-963-121337	Sequence 121337, A
1383	82	6.7	858	14	US-10-099-322-135	Sequence 135, App
1384	82	6.7	858	15	US-10-044-564-135	Sequence 135, App
1385	82	6.7	867	10	US-09-970-944-37	Sequence 37, Appl
1386	82	6.7	867	14	US-10-099-322-134	Sequence 134, App
1387	82	6.7	867	15	US-10-044-564-134	Sequence 134, App
1388	81.5	6.7	261	11	US-09-933-245-1827	Sequence 1827, Ap
1389	81.5	6.7	316	10	US-09-795-271-6	Sequence 6, Appli
1390	81.5	6.7	1694	14	US-10-833-245-1827	Sequence 36, Appl
1391	81.5	6.7	1709	14	US-10-203-708-36	Sequence 35, Appl
1392	81	6.7	461	14	US-10-369-493-5084	Sequence 5084, Ap
1393	80.5	6.6	430	16	US-10-437-963-127004	Sequence 127004, A
1394	80.5	6.6	930	16	US-10-437-963-113209	Sequence 113209, A
1395	80	6.6	607	16	US-10-437-963-121923	Sequence 121923, A
1396	80	6.6	776	17	US-10-425-115-184737	Sequence 184737, A
1397	80	6.6	1055	16	US-10-437-963-147489	Sequence 147489, A
1398	79	6.5	144	15	US-10-108-260A-2843	Sequence 2843, Ap
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1402	79	6.5	1353	9	US-09-751-100B-2	Sequence 2, Appli
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1413	77.5	6.4	434	15	US-10-282-122A-53821	Sequence 53821, A
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1415	77.5	6.4	453	15	US-10-096-625-117	Sequence 117, App
1416	77.5	6.4	456	15	US-10-424-599-262439	Sequence 262439,
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1457	74.5	6.1	654	9	US-09-764-853-494	Sequence 6160, Ap
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1462	74.5	6.1	1709	10	US-09-863-776-60	Sequence 1562, Ap
1463	74.5	6.1	1709	16	US-10-408-765A-1562	Sequence 168, App
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1471	74	6.1	857	14	US-10-099-322-133	Sequence 133, App
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Job time : 184 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 24, 2005, 15:42:36 ; Search time 40 Seconds  
(without alignments)  
379.671 Million cell updates/sec

Title: US-10-063-553-48  
Perfect score: 1215  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Issued Patents AA:\*

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- 3: /cg2\_6/ptodata/1/iaa/6A.COMB.pep:\*
- 4: /cg2\_6/ptodata/1/iaa/6B.COMB.pep:\*
- 5: /cg2\_6/ptodata/1/iaa/PCTUS.COMB.pep:\*
- 6: /cg2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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4	170	14.0	198	3	US-09-227-357-232
5	170	14.0	202	1	US-08-048-700-2
6	170	14.0	202	2	US-08-855-261A-3
7	170	14.0	202	3	US-08-839-711-3
8	170	14.0	202	3	US-09-227-224-3
9	170	14.0	202	4	US-09-855-288-9
10	160	13.2	202	2	US-08-839-711-4
11	160	13.2	202	3	US-08-855-261A-4
12	160	13.2	202	3	US-09-227-224-4
13	160	13.2	202	4	US-09-855-288-10
14	125	10.3	205	3	US-08-839-711-1
15	85.5	7.0	344	1	US-08-889-974-1
16	85.5	7.0	344	3	US-09-058-376-1
17	81	6.7	254	1	US-08-047-413-9
18	81	6.7	254	3	US-08-229-050-9
19	81	6.7	254	3	US-08-801-563-9
20	79.5	6.5	430	3	US-09-134-001C-2981
21	79.5	6.5	1160	4	US-09-328-352-6826
22	79	6.5	315	3	US-09-134-001C-5446
23	79	6.5	555	4	US-09-543-681A-4582
24	79	6.5	1305	3	US-08-864-785-3
25	79	6.5	1353	3	US-08-894-173-2
26	79	6.5	1353	3	US-09-398-193-2
27	78	6.4	1065	4	US-09-252-991A-31637

28	78	6.4	1353	3	US-09-473-717-3	Sequence 3, Appli
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30	76.5	6.3	614	4	US-09-489-039A-12605	Sequence 12605, A
31	76	6.3	337	4	US-09-710-279-444	Sequence 444, App
32	76	6.3	500	4	US-09-543-681A-4601	Sequence 4601, Ap
33	75	6.2	277	4	US-09-328-352-7936	Sequence 7936, Ap
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35	75	6.2	2199	5	PCT-US95-11684-2	Sequence 2, Appli
36	75	6.2	2200	4	US-09-796-575-2	Sequence 2, Appli
37	73.5	6.0	624	4	US-09-543-681A-4343	Sequence 4343, Ap
38	73	6.0	203	4	US-09-252-991A-22678	Sequence 22678, A
39	73	6.0	631	3	US-09-345-468-12	Sequence 12, Appl
40	73	6.0	631	3	US-09-414-453A-12	Sequence 12, Appl
41	72.5	6.0	180	4	US-09-270-767-32589	Sequence 32589, A
42	72.5	6.0	180	4	US-09-270-767-47806	Sequence 47806, A
43	72.5	6.0	616	1	US-08-149-100-2	Sequence 2, Appli
44	72	5.9	296	4	US-09-489-039A-10219	Sequence 10219, A
45	72	5.9	332	4	US-09-270-767-43166	Sequence 43166, A
46	72	5.9	475	4	US-09-543-681A-4458	Sequence 4458, Ap
47	72	5.9	741	4	US-09-248-796A-18963	Sequence 18963, A
48	72	5.9	1253	3	US-08-864-785-2	Sequence 2, Appli
49	71.5	5.9	250	4	US-09-270-767-42724	Sequence 42724, A
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51	71.5	5.9	398	2	US-08-288-663A-1	Sequence 1, Appli
52	71.5	5.9	445	4	US-09-710-279-2644	Sequence 2644, Ap
53	71.5	5.9	450	3	US-09-134-001C-4858	Sequence 4858, Ap
54	71	5.8	299	4	US-09-393-634-5	Sequence 5, Appli
55	70.5	5.8	286	3	US-09-333-521-1	Sequence 1, Appli
56	70.5	5.8	319	4	US-09-543-681A-5398	Sequence 5398, Ap
57	70.5	5.8	600	4	US-09-198-452A-397	Sequence 397, App
58	70	5.8	255	4	US-09-302-62B-76	Sequence 76, Appl
59	70	5.8	485	4	US-09-602-787A-614	Sequence 614, App
60	70	5.8	625	4	US-09-489-039A-10099	Sequence 10099, A
61	70	5.8	715	4	US-09-792-024-85	Sequence 85, Appl
62	70	5.8	735	4	US-09-270-767-40232	Sequence 40232, A
63	70	5.8	735	4	US-09-270-767-55448	Sequence 55448, A
64	70	5.8	797	4	US-09-191-468-120	Sequence 120, App
65	70	5.8	797	4	US-09-191-468-122	Sequence 122, App
66	70	5.8	1058	2	US-08-687-289A-5	Sequence 5, Appli
67	70	5.8	1058	4	US-09-435-897-5	Sequence 21509, A
68	69.5	5.7	172	4	US-09-248-796A-21509	Sequence 14, Appl
69	69.5	5.7	235	4	US-09-472-087-14	Sequence 65, Appl
70	69.5	5.7	235	4	US-09-472-087-65	Sequence 66, Appl
71	69.5	5.7	320	4	US-09-543-681A-6667	Sequence 47, Appl
72	69.5	5.7	347	1	US-08-118-270-47	Sequence 47, Appl
73	69.5	5.7	347	5	PCT-US93-08528-47	Sequence 47, Appl
74	69.5	5.7	1019	4	US-09-252-991A-24417	Sequence 24417, A
75	69	5.7	160	4	US-09-248-796A-24377	Sequence 24377, A
76	69	5.7	245	4	US-09-325-932A-89	Sequence 89, Appl
77	69	5.7	405	2	US-08-700-013B-6	Sequence 6, Appli
78	69	5.7	493	3	US-09-134-001C-3486	Sequence 3486, Ap
79	69	5.7	500	4	US-09-252-991A-25053	Sequence 25053, A
80	69	5.7	797	2	US-08-700-013B-19	Sequence 19, Appl
81	69	5.7	797	3	US-09-182-728A-2	Sequence 2, Appli
82	69	5.7	797	4	US-09-191-468-124	Sequence 124, App
83	69	5.7	797	4	US-09-795-232-2	Sequence 2, Appli
84	69	5.7	2496	3	US-09-125-028-2	Sequence 4112, Ap
85	68.5	5.6	208	4	US-09-583-110-4112	Sequence 4914, Ap
86	68.5	5.6	323	4	US-09-619-353-4	Sequence 2928, Ap
87	68.5	5.6	356	4	US-09-134-000C-4914	Sequence 6175, Ap
88	68.5	5.6	465	4	US-09-107-532A-6175	Sequence 3564, Ap
89	68.5	5.6	467	4	US-09-107-532A-6175	Sequence 458, App
90	68.5	5.6	473	3	US-09-134-001C-3564	Sequence 466, App
91	68.5	5.6	2032	4	US-09-071-035-458	Sequence 6612, Ap
92	68.5	5.6	2032	4	US-09-071-035-462	Sequence 55, Appl
93	68.5	5.6	2032	4	US-09-071-035-466	Sequence 14877, A
94	68.5	5.6	2054	4	US-09-134-000C-6612	Sequence 10551, A
95	68	5.6	205	4	US-09-191-468-55	Sequence 462, App
96	68	5.6	271	4	US-09-248-796A-14877	Sequence 9, Appli
97	68	5.6	320	4	US-09-489-039A-10551	Sequence 276, App
98	68	5.6	354	2	US-08-700-013B-9	
99	68	5.6	443	4	US-09-711-164-462	
100	68	5.6	443	4	US-09-492-709A-276	

101	68	5.6	498	5	PCT-US94-01101-2	Sequence 2, Appli
102	68	5.6	596	2	US-08-392-806A-2	Sequence 2, Appli
103	68	5.6	596	3	US-09-257-490-2	Sequence 2, Appli
104	68	5.6	694	4	US-09-252-991A-22637	Sequence 22637, A
105	68	5.6	797	2	US-08-700-013B-21	Sequence 21, Appl
106	68	5.6	799	2	US-08-700-013B-27	Sequence 27, Appl
107	68	5.6	1810	4	US-08-793-273C-4	Sequence 4, Appli
108	68	5.6	1810	5	PCT-US95-11684-4	Sequence 4, Appli
109	67.5	5.6	155	4	US-09-107-532A-6942	Sequence 6942, Ap
110	67.5	5.6	312	4	US-09-393-634-51	Sequence 51, Appl
111	67.5	5.6	317	2	US-08-619-362A-8	Sequence 8, Appli
112	67.5	5.6	372	4	US-09-252-991A-26719	Sequence 26719, A
113	67.5	5.6	449	4	US-09-543-681A-6546	Sequence 6546, Ap
114	67.5	5.6	2161	1	US-07-745-206A-2	Sequence 2, Appli
115	67.5	5.6	2161	1	US-08-455-543A-49	Sequence 49, Appl
116	67.5	5.6	2161	1	US-08-455-543A-51	Sequence 51, Appl
117	67.5	5.6	2161	2	US-08-223-305C-49	Sequence 49, Appl
118	67.5	5.6	2161	2	US-08-223-305C-51	Sequence 51, Appl
119	67.5	5.6	2161	2	US-08-311-363-2	Sequence 2, Appli
120	67	5.5	147	4	US-09-134-000C-6018	Sequence 6018, Ap
121	67	5.5	167	4	US-09-191-468-65	Sequence 65, Appl
122	67	5.5	199	4	US-09-248-796A-14467	Sequence 14467, A
123	67	5.5	203	4	US-09-270-767-38554	Sequence 38554, A
124	67	5.5	203	4	US-09-270-767-53771	Sequence 53771, A
125	67	5.5	205	4	US-09-191-468-63	Sequence 63, Appl
126	67	5.5	205	4	US-09-191-468-68	Sequence 68, Appl
127	67	5.5	205	4	US-09-191-468-70	Sequence 70, Appl
128	67	5.5	283	4	US-09-134-000C-4870	Sequence 4870, Ap
129	67	5.5	287	4	US-09-252-991A-31548	Sequence 31548, A
130	67	5.5	297	4	US-09-540-236-3296	Sequence 3296, Ap
131	67	5.5	339	4	US-09-328-352-4674	Sequence 4674, Ap
132	67	5.5	342	4	US-09-540-236-2385	Sequence 2385, Ap
133	67	5.5	345	4	US-09-248-796A-26951	Sequence 26951, A
134	67	5.5	376	4	US-09-540-236-3121	Sequence 3121, Ap
135	67	5.5	393	1	US-07-629-1041-3	Sequence 3, Appli
136	67	5.5	448	4	US-09-792-024-101	Sequence 101, App
137	67	5.5	486	4	US-09-178-093B-1	Sequence 1, Appli
138	67	5.5	630	4	US-09-538-092-384	Sequence 384, App
139	67	5.5	1791	4	US-09-354-147C-42	Sequence 2, Appli
140	67	5.5	2958	3	US-08-894-344C-2	Sequence 2, Appli
141	66.5	5.5	280	4	US-09-270-767-32524	Sequence 32524, A
142	66.5	5.5	280	4	US-09-270-767-47741	Sequence 47741, A
143	66.5	5.5	353	3	US-08-838-151A-44	Sequence 44, Appl
144	66.5	5.5	353	3	US-08-838-151A-46	Sequence 46, Appl
145	66.5	5.5	376	4	US-09-404-296B-32	Sequence 32, Appl
146	66.5	5.5	517	4	US-09-540-236-2403	Sequence 2403, Ap
147	66.5	5.5	562	4	US-09-328-352-4694	Sequence 4694, Ap
148	66.5	5.5	585	4	US-09-328-352-6133	Sequence 6133, Ap
149	66.5	5.5	1027	3	US-09-162-021B-2	Sequence 2, Appli
150	66.5	5.5	1027	4	US-10-268-051-8	Sequence 8, Appli
151	66.5	5.5	1078	1	US-08-485-588-7	Sequence 7, Appli
152	66.5	5.5	1078	1	US-08-484-565-7	Sequence 7, Appli
153	66.5	5.5	1078	2	US-08-480-751-7	Sequence 7, Appli
154	66.5	5.5	1078	2	US-08-943-986-7	Sequence 7, Appli
155	66.5	5.5	1078	3	US-08-353-784-7	Sequence 7, Appli
156	66.5	5.5	1078	3	US-08-484-159-7	Sequence 7, Appli
157	66.5	5.5	1078	3	US-08-484-159-7	Sequence 7, Appli
158	66.5	5.5	1088	1	US-08-485-588-6	Sequence 6, Appli
159	66.5	5.5	1088	1	US-08-484-565-6	Sequence 6, Appli
160	66.5	5.5	1088	2	US-08-480-751-6	Sequence 6, Appli
161	66.5	5.5	1088	2	US-08-943-986-6	Sequence 6, Appli
162	66.5	5.5	1088	3	US-08-353-784-6	Sequence 6, Appli
163	66.5	5.5	1088	3	US-08-484-719B-6	Sequence 6, Appli
164	66.5	5.5	1088	3	US-08-484-159-6	Sequence 6, Appli
165	66	5.4	160	4	US-09-270-767-36568	Sequence 36568, A
166	66	5.4	160	4	US-09-270-767-51785	Sequence 51785, A
167	66	5.4	205	4	US-09-191-468-57	Sequence 57, Appl
168	66	5.4	217	4	US-09-270-767-33957	Sequence 33957, A
169	66	5.4	217	4	US-09-270-767-49174	Sequence 49174, A
170	66	5.4	236	4	US-09-598-401C-72	Sequence 72, Appl
171	66	5.4	250	4	US-09-710-279-1124	Sequence 1124, Ap
172	66	5.4	255	4	US-09-302-626B-78	Sequence 78, Appl
173	66	5.4	268	4	US-09-710-279-1830	Sequence 1830, Ap
174	66	5.4	273	3	US-09-134-001C-3917	Sequence 3917, Ap
175	66	5.4	342	4	US-09-054-272-2	Sequence 2, Appli
176	66	5.4	345	4	US-09-602-787A-544	Sequence 544, App
177	66	5.4	352	4	US-09-029-027B-2	Sequence 2, Appli
178	66	5.4	376	4	US-09-710-279-490	Sequence 490, App
179	66	5.4	376	4	US-09-710-279-2260	Sequence 2260, Ap
180	66	5.4	482	1	US-07-792-885A-1	Sequence 1, Appli
181	66	5.4	482	1	US-08-142-439A-7	Sequence 7, Appli
182	66	5.4	482	2	US-08-869-477-7	Sequence 7, Appli
183	66	5.4	594	4	US-09-107-532A-7250	Sequence 7250, Ap
184	66	5.4	718	4	US-09-657-960-3	Sequence 3, Appli
185	66	5.4	877	4	US-09-206-551-20	Sequence 20, Appl
186	66	5.4	1353	3	US-09-398-193-99	Sequence 99, Appl
187	66	5.4	1451	4	US-09-060-299-25	Sequence 25, Appl
188	66	5.4	1451	4	US-09-402-923A-25	Sequence 25, Appl
189	66	5.4	1584	4	US-09-060-299-39	Sequence 39, Appl
190	66	5.4	1584	4	US-09-402-923A-39	Sequence 39, Appl
191	66	5.4	1591	4	US-09-060-299-4	Sequence 4, Appli
192	66	5.4	1591	4	US-09-060-299-43	Sequence 43, Appl
193	66	5.4	1591	4	US-09-402-923A-4	Sequence 4, Appli
194	66	5.4	1591	4	US-09-402-923A-43	Sequence 43, Appl
195	66	5.4	1615	4	US-09-060-299-3	Sequence 3, Appli
196	66	5.4	1615	4	US-09-402-923A-3	Sequence 3, Appli
197	66	5.4	1615	4	US-09-544-398B-3	Sequence 3, Appli
198	66	5.4	1615	4	US-09-544-398B-4	Sequence 4, Appli
199	66	5.4	1615	4	US-09-543-771-3	Sequence 3, Appli
200	66	5.4	1615	4	US-09-543-771-4	Sequence 4, Appli
201	66	5.4	1639	4	US-09-060-299-29	Sequence 29, Appl
202	66	5.4	1639	4	US-09-402-923A-29	Sequence 29, Appl
203	65.5	5.4	176	4	US-09-252-991A-25290	Sequence 25290, A
204	65.5	5.4	268	3	US-08-965-056-70	Sequence 70, Appl
205	65.5	5.4	318	2	US-08-619-362A-9	Sequence 9, Appli
206	65.5	5.4	353	3	US-08-838-151A-52	Sequence 52, Appl
207	65.5	5.4	353	3	US-08-838-151A-55	Sequence 55, Appl
208	65.5	5.4	398	4	US-09-543-681A-5507	Sequence 5507, Ap
209	65.5	5.4	536	4	US-09-107-532A-5507	Sequence 5507, Ap
210	65.5	5.4	650	1	US-08-121-713D-60	Sequence 60, Appl
211	65.5	5.4	650	1	US-08-835-268-60	Sequence 60, Appl
212	65.5	5.4	650	2	US-09-060-692-60	Sequence 60, Appl
213	65.5	5.4	650	3	US-08-833-391-60	Sequence 60, Appl
214	65.5	5.4	650	3	US-09-060-610-60	Sequence 60, Appl
215	65.5	5.4	650	5	PCT-US94-10151A-60	Sequence 20611, A
216	65.5	5.4	1033	4	US-09-252-991A-20611	Sequence 20611, A
217	65.5	5.4	1058	4	US-09-328-352-4276	Sequence 4276, Ap
218	65.5	5.4	1085	1	US-08-485-588-5	Sequence 5, Appli
219	65.5	5.4	1085	1	US-08-484-565-5	Sequence 5, Appli
220	65.5	5.4	1085	2	US-08-480-751-5	Sequence 5, Appli
221	65.5	5.4	1085	2	US-08-943-986-5	Sequence 5, Appli
222	65.5	5.4	1085	3	US-08-353-784-5	Sequence 5, Appli
223	65.5	5.4	1085	3	US-08-484-719B-5	Sequence 5, Appli
224	65.5	5.4	1085	3	US-08-484-159-5	Sequence 5, Appli
225	65.5	5.4	1621	3	US-08-972-927-3	Sequence 3, Appli
226	65	5.3	88	4	US-09-621-976-5007	Sequence 5007, Ap
227	65	5.3	105	4	US-09-489-039A-11705	Sequence 11705, A
228	65	5.3	289	4	US-09-489-039A-12627	Sequence 12627, A
229	65	5.3	367	4	US-09-543-681A-4184	Sequence 4184, Ap
230	65	5.3	434	4	US-09-328-352-4563	Sequence 4563, Ap
231	65	5.3	491	4	US-09-543-681A-8251	Sequence 8251, Ap
232	65	5.3	509	2	US-09-031-392-6	Sequence 6, Appli
233	65	5.3	509	3	US-09-299-549-6	Sequence 6, Appli
234	65	5.3	509	3	US-09-610-417-6	Sequence 6, Appli
235	65	5.3	580	2	US-08-677-049-12	Sequence 12, Appl
236	65	5.3	749	4	US-09-562-737-97	Sequence 97, Appl
237	65	5.3	863	4	US-09-894-927B-9	Sequence 9, Appli
238	64.5	5.3	186	4	US-09-248-796A-24150	Sequence 24150, A
239	64.5	5.3	190	4	US-09-543-681A-8168	Sequence 8168, Ap
240	64.5	5.3	230	4	US-09-270-767-44365	Sequence 44365, A
241	64.5	5.3	253	1	US-08-162-475A-5	Sequence 5, Appli
242	64.5	5.3	258	4	US-09-248-796A-25815	Sequence 25815, A
243	64.5	5.3	282	4	US-09-247-890-16	Sequence 16, Appl
244	64.5	5.3	282	4	US-09-724-969-16	Sequence 16, Appl
245	64.5	5.3	282	4	US-09-724-852-16	Sequence 16, Appl
246	64.5	5.3	317	2	US-08-790-572-3	Sequence 3, Appli

247	64.5	5.3	317	2	US-09-213-398-3	Sequence 3, Appli	320	63	5.2	458	3	US-09-292-069A-29	Sequence 29, Appl
248	64.5	5.3	327	3	US-08-748-506-22	Sequence 22, Appl	321	63	5.2	458	3	US-09-032-742-10	Sequence 10, Appl
249	64.5	5.3	327	3	US-08-748-506-23	Sequence 23, Appl	322	63	5.2	458	4	US-09-767-013-27	Sequence 27, Appl
250	64.5	5.3	331	4	US-09-830-217-18	Sequence 18, Appl	323	63	5.2	458	4	US-09-767-013-29	Sequence 29, Appl
251	64.5	5.3	338	4	US-09-252-991A-27402	Sequence 27402, A	324	63	5.2	458	4	US-09-341-446B-11	Sequence 11, Appl
252	64.5	5.3	615	2	US-08-663-566A-17	Sequence 17, Appl	325	63	5.2	458	4	US-09-292-072-27	Sequence 27, Appl
253	64.5	5.3	615	2	US-08-023-610-17	Sequence 17, Appl	326	63	5.2	458	4	US-09-292-072-29	Sequence 29, Appl
254	64.5	5.3	615	2	US-08-288-065A-17	Sequence 17, Appl	327	63	5.2	458	4	US-09-170-496D-126	Sequence 126, App
255	64.5	5.3	615	2	US-08-352-240A-17	Sequence 17, Appl	328	63	5.2	458	4	US-09-170-496D-230	Sequence 230, App
256	64.5	5.3	615	5	PCT-US95-10245-17	Sequence 17, Appl	329	63	5.2	531	4	US-09-248-796A-16160	Sequence 16160, A
257	64.5	5.3	620	1	US-08-311-722A-2	Sequence 2, Appli	330	63	5.2	532	3	US-09-117-853-2	Sequence 2, Appli
258	64.5	5.3	718	4	US-09-252-991A-28229	Sequence 28229, A	331	63	5.2	532	4	US-09-911-154-2	Sequence 2, Appli
259	64.5	5.3	1580	3	US-08-726-320-1	Sequence 1, Appli	332	63	5.2	532	4	US-09-485-529-2	Sequence 2, Appli
260	64.5	5.3	1580	3	US-09-208-716-1	Sequence 4, Appli	333	63	5.2	532	4	US-09-911-514-2	Sequence 2, Appli
261	64.5	5.3	3177	2	US-08-477-451-4	Sequence 6, Appli	334	63	5.2	556	4	US-09-538-092-712	Sequence 712, App
262	64	5.3	167	2	US-08-627-610-6	Sequence 46, Appl	335	63	5.2	571	4	US-09-973-180A-2	Sequence 3, Appli
263	64	5.3	168	2	US-08-508-735-46	Sequence 46, Appl	336	63	5.2	571	4	US-09-973-180A-3	Sequence 4, Appli
264	64	5.3	168	3	US-09-201-139-46	Sequence 5992, Ap	337	63	5.2	571	4	US-09-973-180A-4	Sequence 4, Appli
265	64	5.3	195	4	US-09-134-000C-5992	Sequence 61, Appl	338	63	5.2	606	3	US-09-041-236-4	Sequence 4, Appli
266	64	5.3	205	4	US-09-191-468-61	Sequence 6839, Ap	339	63	5.2	606	4	US-09-771-467C-4	Sequence 107, App
267	64	5.3	322	4	US-09-533-681A-6839	Sequence 22533, A	340	63	5.2	682	1	US-07-998-003A-107	Sequence 107, App
268	64	5.3	379	4	US-09-248-796A-22533	Sequence 6174, Ap	341	63	5.2	682	1	US-08-453-274B-107	Sequence 107, App
269	64	5.3	456	4	US-09-328-352-6174	Sequence 7797, Ap	342	63	5.2	682	1	US-08-453-695A-107	Sequence 107, App
270	64	5.3	484	4	US-09-328-352-7797	Sequence 7690, Ap	343	63	5.2	682	2	US-08-268-161A-107	Sequence 107, App
271	64	5.3	484	4	US-09-409-039A-7690	Sequence 32124, A	344	63	5.2	682	2	US-08-453-702A-107	Sequence 107, App
272	64	5.3	579	4	US-09-252-991A-32124	Sequence 17196, A	345	63	5.2	682	3	US-09-099-639-107	Sequence 107, App
273	64	5.3	808	4	US-09-288-796A-17196	Sequence 7, Appli	346	63	5.2	682	5	PCT-US93-12588-107	Sequence 107, App
274	64	5.3	1182	3	US-09-293-505-7	Sequence 7, Appli	347	63	5.2	682	5	PCT-US95-08071-107	Sequence 107, App
275	64	5.3	1182	4	US-09-060-939A-7	Sequence 2, Appli	348	63	5.2	804	4	US-09-270-767-46146	Sequence 46146, A
276	64	5.3	1203	3	US-09-293-505-2	Sequence 2, Appli	349	63	5.2	836	1	US-07-998-003A-105	Sequence 105, App
277	64	5.3	1203	4	US-09-060-939A-2	Sequence 21678, A	350	63	5.2	836	1	US-08-453-274B-105	Sequence 105, App
278	63.5	5.2	178	4	US-09-248-796A-21678	Sequence 20685, A	351	63	5.2	836	1	US-08-453-695A-105	Sequence 105, App
279	63.5	5.2	211	4	US-09-248-796A-20685	Sequence 608, App	352	63	5.2	836	2	US-08-453-702A-105	Sequence 105, App
280	63.5	5.2	220	4	US-09-602-787A-608	Sequence 79, Appl	353	63	5.2	836	3	US-09-099-639-105	Sequence 105, App
281	63.5	5.2	236	4	US-09-315-926A-79	Sequence 7537, Ap	354	63	5.2	836	3	PCT-US93-12588-105	Sequence 105, App
282	63.5	5.2	240	4	US-09-328-352-7537	Sequence 71, Appl	355	63	5.2	836	5	PCT-US95-08071-105	Sequence 105, App
283	63.5	5.2	268	3	US-08-965-056-71	Sequence 32358, A	356	63	5.2	836	5	US-07-998-003A-97	Sequence 97, Appl
284	63.5	5.2	350	4	US-09-252-991A-32358	Sequence 15, Appl	357	63	5.2	904	1	US-08-453-274B-97	Sequence 97, Appl
285	63.5	5.2	398	2	US-08-288-663A-15	Sequence 9, Appli	358	63	5.2	904	1	US-08-453-695A-97	Sequence 97, Appl
286	63.5	5.2	400	2	US-08-103-170-9	Sequence 606, App	359	63	5.2	904	1	US-08-268-161A-97	Sequence 97, Appl
287	63.5	5.2	403	4	US-09-602-787A-606	Sequence 5746, Ap	360	63	5.2	904	2	US-08-453-702A-97	Sequence 97, Appl
288	63.5	5.2	433	4	US-09-328-352-5746	Sequence 3794, Ap	361	63	5.2	904	2	US-08-453-702A-97	Sequence 97, Appl
289	63.5	5.2	448	4	US-09-134-000C-3794	Sequence 6048, Ap	362	63	5.2	904	5	PCT-US93-12588-97	Sequence 97, Appl
290	63.5	5.2	467	4	US-09-540-236-2469	Sequence 2469, Ap	363	63	5.2	904	5	PCT-US95-08071-97	Sequence 97, Appl
291	63.5	5.2	482	4	US-09-107-532A-6644	Sequence 6644, Ap	364	63	5.2	1233	4	US-09-354-147C-7	Sequence 7, Appli
292	63.5	5.2	575	4	US-09-248-796A-20353	Sequence 20353, A	365	63	5.2	1243	4	US-09-354-147C-8	Sequence 8, Appli
293	63.5	5.2	590	4	US-09-248-796A-18826	Sequence 18826, A	366	63	5.2	1294	3	US-09-473-717-2	Sequence 2, Appli
294	63.5	5.2	2957	4	US-09-252-991A-24252	Sequence 24252, A	367	63	5.2	3119	1	US-08-246-982A-16	Sequence 16, Appl
295	63.5	5.2	1179	4	US-09-792-024-89	Sequence 89, Appl	368	63	5.2	3119	1	US-08-453-265-16	Sequence 16, Appl
296	63.5	5.2	103	4	US-09-248-796A-27772	Sequence 27772, A	369	63	5.1	138	4	US-09-248-796A-24261	Sequence 24261, A
297	63	5.2	210	4	US-09-710-279-708	Sequence 140175, A	370	62.5	5.1	152	4	US-09-270-767-47052	Sequence 47052, A
298	63	5.2	216	4	US-09-248-796A-14175	Sequence 4608, Ap	371	62.5	5.1	185	4	US-09-270-767-34409	Sequence 34409, A
299	63	5.2	224	3	US-09-134-001C-4608	Sequence 13172, A	372	62.5	5.1	222	4	US-09-270-767-49626	Sequence 49626, A
300	63	5.2	275	4	US-09-409-039A-13172	Sequence 5, Appli	373	62.5	5.1	269	2	US-08-484-905-116	Sequence 116, App
301	63	5.2	295	2	US-08-679-765-5	Sequence 5, Appli	374	62.5	5.1	269	3	US-08-481-985B-116	Sequence 116, App
302	63	5.2	295	3	US-09-196-525-5	Sequence 22, Appl	375	62.5	5.1	269	3	US-08-370-476-116	Sequence 116, App
303	63	5.2	295	4	US-09-177-165A-22	Sequence 137, App	376	62.5	5.1	270	4	US-09-270-767-46312	Sequence 46312, A
304	63	5.2	295	4	US-09-538-092-137	Sequence 6394, Ap	377	62.5	5.1	281	4	US-09-270-767-58184	Sequence 58184, A
305	63	5.2	341	4	US-09-134-000C-6394	Sequence 31716, A	378	62.5	5.1	282	3	US-09-117-853-8	Sequence 8, Appli
306	63	5.2	356	4	US-09-252-991A-31716	Sequence 10, Appl	379	62.5	5.1	282	4	US-09-911-154-8	Sequence 8, Appli
307	63	5.2	364	4	US-08-758-621-10	Sequence 10, Appl	380	62.5	5.1	282	4	US-09-911-154-8	Sequence 8, Appli
308	63	5.2	376	2	US-09-107-858-10	Sequence 10, Appl	381	62.5	5.1	282	4	US-09-911-154-8	Sequence 8, Appli
309	63	5.2	376	3	US-09-579-174-10	Sequence 4615, Ap	382	62.5	5.1	315	4	US-10-090-190-3	Sequence 3, Appli
310	63	5.2	391	4	US-09-107-532A-4615	Sequence 18502, A	383	62.5	5.1	315	4	US-10-090-190-6	Sequence 3, Appli
311	63	5.2	394	4	US-09-252-991A-18502	Sequence 6669, Ap	384	62.5	5.1	315	4	US-10-082-902-3	Sequence 3, Appli
312	63	5.2	445	4	US-09-328-352-6669	Sequence 2, Appli	385	62.5	5.1	315	4	US-10-082-902-6	Sequence 3, Appli
313	63	5.2	458	1	US-08-310-271-2	Sequence 27, Appl	386	62.5	5.1	315	4	US-09-370-398-6	Sequence 3, Appli
314	63	5.2	458	3	US-09-292-071-27	Sequence 29, Appl	387	62.5	5.1	315	4	US-09-370-398-3	Sequence 3, Appli
315	63	5.2	458	3	US-09-292-071-29	Sequence 27, Appl	388	62.5	5.1	315	4	US-09-370-398-3	Sequence 3, Appli
316	63	5.2	458	3	US-09-292-071-29	Sequence 27, Appl	389	62.5	5.1	315	4	US-09-370-398-3	Sequence 3, Appli
317	63	5.2	458	3	US-09-292-071-29	Sequence 27, Appl	390	62.5	5.1	315	4	US-09-370-398-3	Sequence 3, Appli
318	63	5.2	458	3	US-09-292-071-29	Sequence 27, Appl	391	62.5	5.1	315	4	US-09-370-398-3	Sequence 3, Appli
319	63	5.2	458	3	US-09-292-071-29	Sequence 27, Appl	392	62.5	5.1	315	4	US-09-370-398-3	Sequence 3, Appli



393	62.5	5.1	342	3	US-08-785-928-1	Sequence 1, Appli	466	61.5	5.1	249	4	US-09-328-352-6476	Sequence 6476, Ap
394	62.5	5.1	342	3	US-08-728-603-17	Sequence 17, Appli	467	61.5	5.1	267	4	US-09-134-000C-5723	Sequence 5723, Ap
395	62.5	5.1	383	4	US-09-704-725-7	Sequence 7, Appli	468	61.5	5.1	268	4	US-09-248-796A-18304	Sequence 18304, A
396	62.5	5.1	386	3	US-09-086-483A-2	Sequence 2, Appli	469	61.5	5.1	298	4	US-09-134-000C-5845	Sequence 5845, Ap
397	62.5	5.1	386	4	US-09-130-491-6	Sequence 6, Appli	470	61.5	5.1	317	3	US-09-134-001C-5199	Sequence 5199, Ap
398	62.5	5.1	386	4	US-09-580-212-2	Sequence 2, Appli	471	61.5	5.1	326	1	US-08-118-270-39	Sequence 39, Appl
399	62.5	5.1	386	4	US-09-769-402-2	Sequence 2, Appli	472	61.5	5.1	326	5	PCT-US93-08528-39	Sequence 39, Appl
400	62.5	5.1	386	4	US-10-140-002-340	Sequence 340, App	473	61.5	5.1	355	4	US-09-489-039A-9302	Sequence 9302, Ap
401	62.5	5.1	405	4	US-09-543-681A-6109	Sequence 6109, Ap	474	61.5	5.1	370	1	US-08-118-270-18	Sequence 18, Appl
402	62.5	5.1	446	4	US-09-328-352-7464	Sequence 7464, Ap	475	61.5	5.1	370	5	PCT-US93-08528-18	Sequence 18, Appl
403	62.5	5.1	478	4	US-09-489-039A-12376	Sequence 12376, A	476	61.5	5.1	488	4	US-09-248-796A-16184	Sequence 16184, A
404	62.5	5.1	485	4	US-09-328-352-8210	Sequence 8210, Ap	477	61.5	5.1	496	4	US-09-489-039A-8772	Sequence 8772, Ap
405	62.5	5.1	486	4	US-09-270-767-42864	Sequence 42864, A	478	61.5	5.1	497	4	US-09-718-693A-1	Sequence 1, Appli
406	62.5	5.1	491	4	US-09-248-796A-22333	Sequence 22333, A	479	61.5	5.1	502	4	US-09-134-000C-6114	Sequence 6114, Ap
407	62.5	5.1	495	4	US-09-252-991A-31450	Sequence 31450, A	480	61.5	5.1	524	4	US-08-529-654-4	Sequence 4, Appli
408	62.5	5.1	526	4	US-09-252-991A-23462	Sequence 23462, A	481	61.5	5.1	542	4	US-09-449-632-4	Sequence 4, Appli
409	62.5	5.1	591	4	US-09-248-796A-14458	Sequence 14458, A	482	61.5	5.1	780	4	US-09-785-381-11	Sequence 11, Appl
410	62.5	5.1	711	4	US-09-134-000C-5325	Sequence 5325, Ap	483	61.5	5.1	826	4	US-09-134-000C-4999	Sequence 4999, Ap
411	62.5	5.1	716	3	US-08-971-188-11	Sequence 11, Appl	484	61.5	5.1	1059	3	US-09-134-513-2	Sequence 2, Appli
412	62.5	5.1	851	4	US-09-543-681A-7277	Sequence 7277, Ap	485	61	5.0	83	4	US-09-621-976-4085	Sequence 4085, Ap
413	62.5	5.1	879	1	US-08-554-612C-1	Sequence 1, Appli	486	61	5.0	108	4	US-09-471-803A-5	Sequence 5, Appli
414	62.5	5.1	1079	1	US-08-485-588-8	Sequence 8, Appli	487	61	5.0	135	4	US-09-270-767-34805	Sequence 34805, A
415	62.5	5.1	1079	2	US-08-484-565-8	Sequence 8, Appli	488	61	5.0	135	4	US-09-270-767-50022	Sequence 50022, A
416	62.5	5.1	1079	2	US-08-480-751-8	Sequence 8, Appli	489	61	5.0	174	3	US-09-383-586-12	Sequence 12, Appl
417	62.5	5.1	1079	2	US-08-943-986-8	Sequence 8, Appli	490	61	5.0	174	4	US-09-823-038A-12	Sequence 13, Appl
418	62.5	5.1	1079	3	US-08-353-784-8	Sequence 8, Appli	491	61	5.0	199	3	US-08-737-248-13	Sequence 13, Appl
419	62.5	5.1	1079	3	US-08-484-719B-8	Sequence 8, Appli	492	61	5.0	203	4	US-09-248-796A-16898	Sequence 16898, A
420	62.5	5.1	1079	3	US-08-484-159-8	Sequence 8, Appli	493	61	5.0	213	3	US-08-807-300-4	Sequence 4, Appli
421	62.5	5.1	1881	3	US-09-233-086-3	Sequence 3, Appli	494	61	5.0	219	4	US-08-311-731A-305	Sequence 305, App
422	62	5.1	113	4	US-09-328-352-7133	Sequence 7133, A	495	61	5.0	221	4	US-09-205-258-1129	Sequence 1129, Ap
423	62	5.1	137	4	US-09-252-991A-29023	Sequence 29023, A	496	61	5.0	220	4	US-09-248-796A-15458	Sequence 15458, A
424	62	5.1	150	3	US-08-862-124-5	Sequence 5, Appli	497	61	5.0	234	4	US-09-472-087-17	Sequence 17, Appl
425	62	5.1	185	3	US-09-324-910-6	Sequence 6, Appli	498	61	5.0	234	4	US-09-472-087-69	Sequence 69, Appl
426	62	5.1	185	4	US-09-793-495-6	Sequence 6, Appli	499	61	5.0	255	4	US-09-107-532A-4920	Sequence 4920, Ap
427	62	5.1	216	4	US-09-294-298A-7	Sequence 7, Appli	500	61	5.0	296	4	US-09-270-767-37980	Sequence 37980, A
428	62	5.1	230	4	US-09-663-600A-186	Sequence 186, App	501	61	5.0	296	4	US-09-270-767-53197	Sequence 53197, A
429	62	5.1	230	4	US-10-140-002-492	Sequence 492, App	502	61	5.0	297	4	US-09-489-039A-8466	Sequence 8466, Ap
430	62	5.1	261	4	US-09-248-796A-18760	Sequence 18760, A	503	61	5.0	299	4	US-09-252-991A-17878	Sequence 17878, A
431	62	5.1	266	4	US-09-540-236-2374	Sequence 2374, Ap	504	61	5.0	300	4	US-09-134-000C-3733	Sequence 3733, Ap
432	62	5.1	287	1	US-08-433-783-37	Sequence 37, Appl	505	61	5.0	308	4	US-09-252-991A-23958	Sequence 23958, A
433	62	5.1	287	2	US-08-337-358-37	Sequence 37, Appl	506	61	5.0	325	4	US-09-461-325-141	Sequence 141, App
434	62	5.1	287	5	PCT-US95-07537A-37	Sequence 37, Appl	507	61	5.0	325	4	US-10-012-542-141	Sequence 141, App
435	62	5.1	287	5	PCT-US95-07537-37	Sequence 37, Appl	508	61	5.0	325	4	US-10-115-123-141	Sequence 5, Appli
436	62	5.1	290	4	US-09-252-991A-18337	Sequence 18337, A	509	61	5.0	365	4	US-09-801-874-5	Sequence 4209, Ap
437	62	5.1	294	1	US-08-628-291-2	Sequence 2, Appli	510	61	5.0	391	4	US-09-107-532A-4209	Sequence 46, Appl
438	62	5.1	294	2	US-09-128-722-2	Sequence 2, Appli	511	61	5.0	426	4	US-09-491-577-46	Sequence 17254, A
439	62	5.1	294	4	US-09-326-157-1	Sequence 1, Appli	512	61	5.0	435	4	US-09-252-991A-17254	Sequence 32306, A
440	62	5.1	294	4	US-10-135-755-1	Sequence 1, Appli	513	61	5.0	441	4	US-09-252-991A-32306	Sequence 6579, Ap
441	62	5.1	302	4	US-09-270-767-40028	Sequence 40028, A	514	61	5.0	446	4	US-09-543-681A-6579	Sequence 8916, Ap
442	62	5.1	302	4	US-09-270-767-55244	Sequence 55244, A	515	61	5.0	453	4	US-09-489-039A-8916	Sequence 26, Appl
443	62	5.1	318	1	US-08-628-291-16	Sequence 16, Appl	516	61	5.0	460	4	US-09-543-681A-8195	Sequence 8246, Ap
444	62	5.1	318	2	US-09-128-722-16	Sequence 12, Appl	517	61	5.0	494	3	US-09-126-420A-26	Sequence 5958, Ap
445	62	5.1	319	3	US-09-324-910-12	Sequence 12, Appl	518	61	5.0	506	4	US-09-543-681A-8246	Sequence 36, Appl
446	62	5.1	319	4	US-09-793-495-12	Sequence 12, Appl	519	61	5.0	518	4	US-09-248-796A-20772	Sequence 2, Appli
447	62	5.1	341	4	US-09-248-796A-20844	Sequence 20844, A	520	61	5.0	529	3	US-09-500-063-2	Sequence 5958, Ap
448	62	5.1	377	4	US-09-248-796A-15498	Sequence 15498, A	521	61	5.0	568	4	US-09-543-681A-5958	Sequence 36, Appl
449	62	5.1	399	4	US-09-489-039A-8272	Sequence 8272, Ap	522	61	5.0	574	3	US-09-383-586-36	Sequence 17469, A
450	62	5.1	409	4	US-09-248-796A-14863	Sequence 14863, A	523	61	5.0	574	4	US-09-823-038A-36	Sequence 31, Appl
451	62	5.1	409	4	US-09-583-110-4040	Sequence 4040, A	524	61	5.0	595	4	US-09-720-317A-31	Sequence 19, Appl
452	62	5.1	516	4	US-09-489-039A-12893	Sequence 12893, A	525	61	5.0	685	4	US-09-206-551-19	Sequence 293, App
453	62	5.1	631	3	US-09-310-463-20	Sequence 20, Appl	526	61	5.0	852	4	US-09-170-496D-293	Sequence 58, Appl
454	62	5.1	631	4	US-08-842-248A-20	Sequence 21, Appl	527	61	5.0	1279	4	US-09-364-425B-58	Sequence 6, Appli
455	62	5.1	1135	4	US-09-294-298A-21	Sequence 6, Appli	528	61	5.0	1279	4	US-09-354-147C-5	Sequence 58664, A
456	62	5.1	1325	4	US-09-294-298A-6	Sequence 4, Appli	529	61	5.0	1765	4	US-08-477-451-6	Sequence 342, App
457	62	5.1	1376	4	US-09-294-298A-4	Sequence 2, Appli	530	61	5.0	3169	2	US-08-311-731A-342	Sequence 4128, Ap
458	62	5.1	1423	4	US-09-294-298A-2	Sequence 8, Appli	531	60.5	5.0	102	4	US-09-621-976-4128	Sequence 19348, A
459	62	5.1	3118	2	US-08-457-273B-8	Sequence 5110, Ap	532	60.5	5.0	117	4	US-09-248-796A-19348	Sequence 2944, Ap
460	61.5	5.1	78	4	US-09-543-681A-5110	Sequence 5881.1, A	533	60.5	5.0	142	4	US-08-965-056-42	Sequence 18429, A
461	61.5	5.1	86	4	US-09-270-767-58811	Sequence 45975, A	534	60.5	5.0	162	4	US-09-134-001C-4741	Patent No. 5482709
462	61.5	5.1	148	4	US-09-270-767-45975	Sequence 1354, Ap	535	60.5	5.0	202	4	US-09-252-991A-18429	
463	61.5	5.1	182	4	US-09-710-279-1354	Sequence 4741, Ap	536	60.5	5.0	269	3		
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465	61.5	5.1	205	6	5482709-4		538	60.5	5.0	369	4		

539	60.5	5.0	381	4	US-09-248-796A-19481	Sequence 19481, A	612	59.5	4.9	243	3	US-08-965-056-73	Sequence 73, Appl
540	60.5	5.0	390	4	US-09-198-452A-254	Sequence 254, App	613	59.5	4.9	279	4	US-09-248-796A-25140	Sequence 25140, A
541	60.5	5.0	424	4	US-09-252-991A-18895	Sequence 18895, A	614	59.5	4.9	329	4	US-09-198-452A-363	Sequence 363, App
542	60.5	5.0	448	4	US-09-361-443-4	Sequence 4, Appli	615	59.5	4.9	337	3	US-08-448-722A-2	Sequence 2, Appli
543	60.5	5.0	467	4	US-09-361-443-2	Sequence 2, Appli	616	59.5	4.9	337	3	US-08-189-309B-2	Sequence 2, Appli
544	60.5	5.0	469	4	US-09-198-452A-793	Sequence 793, App	617	59.5	4.9	373	4	US-09-134-000C-4099	Sequence 4099, Ap
545	60.5	5.0	533	4	US-09-107-532A-5244	Sequence 5244, Ap	618	59.5	4.9	406	4	US-09-489-039A-8267	Sequence 8267, Ap
546	60.5	5.0	681	3	US-08-760-615-4	Sequence 4, Appli	619	59.5	4.9	419	4	US-09-489-039A-12928	Sequence 12928, A
547	60.5	5.0	681	4	US-09-336-910A-2	Sequence 2, Appli	620	59.5	4.9	427	4	US-09-252-991A-31904	Sequence 31904, A
548	60.5	5.0	805	3	US-08-989-299-2	Sequence 2, Appli	621	59.5	4.9	470	4	US-09-543-681A-4625	Sequence 4625, Ap
549	60.5	5.0	805	4	US-10-158-847-142	Sequence 142, App	622	59.5	4.9	477	4	US-09-134-000C-6123	Sequence 6123, Ap
550	60.5	5.0	805	4	US-09-407-427-2	Sequence 2, Appli	623	59.5	4.9	480	2	US-08-724-394A-11	Sequence 11, Appl
551	60.5	5.0	905	1	US-08-072-574-2	Sequence 2, Appli	624	59.5	4.9	483	2	US-08-307-485A-1	Sequence 1, Appli
552	60	4.9	87	4	US-09-252-991A-30361	Sequence 30361, A	625	59.5	4.9	483	2	US-08-465-809-2	Sequence 2, Appli
553	60	4.9	87	4	US-09-107-532A-6457	Sequence 6457, Ap	626	59.5	4.9	483	3	US-08-477-928A-2	Sequence 2, Appli
554	60	4.9	125	4	US-09-198-452A-1172	Sequence 1172, Ap	627	59.5	4.9	483	3	US-08-477-928A-40	Sequence 40, Appl
555	60	4.9	141	4	US-09-198-452A-1173	Sequence 1173, Ap	628	59.5	4.9	555	4	US-09-270-767-43300	Sequence 43300, A
556	60	4.9	158	4	US-09-270-767-38728	Sequence 38728, A	629	59.5	4.9	562	4	US-09-328-352-4802	Sequence 4802, Ap
557	60	4.9	158	4	US-09-270-767-53945	Sequence 53945, A	630	59.5	4.9	563	4	US-09-535-315-23	Sequence 23, Appl
558	60	4.9	205	4	US-09-191-468-59	Sequence 59, Appl	631	59.5	4.9	577	1	US-07-820-154A-30	Sequence 30, Appl
559	60	4.9	211	4	US-09-130-491-4	Sequence 4, Appli	632	59.5	4.9	577	2	US-08-663-566A-11	Sequence 11, Appl
560	60	4.9	211	4	US-09-603-552-12	Sequence 12, Appl	633	59.5	4.9	577	2	US-08-097-554A-30	Sequence 30, Appl
561	60	4.9	211	4	US-09-886-683A-4	Sequence 4, Appli	634	59.5	4.9	577	2	US-08-023-610-11	Sequence 11, Appl
562	60	4.9	214	4	US-09-489-039A-12637	Sequence 12637, A	635	59.5	4.9	577	2	US-08-288-065A-11	Sequence 11, Appl
563	60	4.9	218	4	US-09-252-991A-22136	Sequence 22136, A	636	59.5	4.9	577	2	US-08-362-240A-11	Sequence 11, Appl
564	60	4.9	227	1	US-08-254-493-1	Sequence 1, Appli	637	59.5	4.9	577	3	US-08-480-640A-30	Sequence 30, Appl
565	60	4.9	227	2	US-08-253-751-6	Sequence 6, Appli	638	59.5	4.9	577	3	US-08-295-802-30	Sequence 30, Appl
566	60	4.9	227	2	US-08-453-925-6	Sequence 6, Appli	639	59.5	4.9	577	3	US-08-804-372A-9	Sequence 9, Appli
567	60	4.9	227	3	US-08-403-253A-6	Sequence 6, Appli	640	59.5	4.9	577	3	US-08-488-237A-30	Sequence 30, Appl
568	60	4.9	227	4	US-08-435-816A-6	Sequence 6, Appli	641	59.5	4.9	577	3	US-08-375-992A-30	Sequence 30, Appl
569	60	4.9	228	1	US-08-408-222B-1	Sequence 1, Appli	642	59.5	4.9	577	4	US-08-472-679H-30	Sequence 30, Appl
570	60	4.9	233	2	US-09-024-848-4	Sequence 4, Appli	643	59.5	4.9	577	5	PCT-US93-00324-30	Sequence 30, Appl
571	60	4.9	233	3	US-09-348-116A-4	Sequence 4, Appli	644	59.5	4.9	577	5	PCT-US95-10245-11	Sequence 11, Appl
572	60	4.9	239	4	US-09-270-767-44514	Sequence 44514, A	645	59.5	4.9	581	2	US-08-484-575A-13	Sequence 13, Appl
573	60	4.9	259	4	US-09-270-767-38568	Sequence 38568, A	646	59.5	4.9	581	3	US-08-477-459-13	Sequence 13, Appl
574	60	4.9	259	4	US-09-270-767-53785	Sequence 53785, A	647	59.5	4.9	581	3	US-08-479-869-13	Sequence 13, Appl
575	60	4.9	275	4	US-09-270-767-48250	Sequence 48250, A	648	59.5	4.9	581	3	US-08-486-414-13	Sequence 13, Appl
576	60	4.9	329	4	US-09-604-957-2	Sequence 2, Appli	649	59.5	4.9	581	5	PCT-US94-01826A-13	Sequence 13, Appl
577	60	4.9	365	3	US-08-155-005A-8	Sequence 8, Appli	650	59.5	4.9	581	5	PCT-US94-02252A-13	Sequence 13, Appl
578	60	4.9	365	3	US-09-363-783-8	Sequence 8, Appli	651	59.5	4.9	586	4	US-09-583-110-3470	Sequence 16, Appl
579	60	4.9	365	4	US-09-661-758A-8	Sequence 8, Appli	652	59.5	4.9	621	4	US-09-720-317A-16	Sequence 26, Appl
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581	60	4.9	388	3	US-09-363-783-6	Sequence 6, Appli	654	59.5	4.9	658	4	US-09-720-317A-24	Sequence 138, App
582	60	4.9	388	4	US-09-661-758A-6	Sequence 6, Appli	655	59.5	4.9	711	4	US-10-158-847-138	Sequence 4629, Ap
583	60	4.9	390	3	US-08-155-005A-4	Sequence 4, Appli	656	59.5	4.9	717	4	US-09-583-110-4629	Sequence 4, Appli
584	60	4.9	390	3	US-08-155-005A-17	Sequence 17, Appl	657	59.5	4.9	746	4	US-09-548-797B-4	Sequence 1197, Ap
585	60	4.9	390	3	US-09-363-783-4	Sequence 4, Appli	658	59.5	4.9	940	4	US-09-489-039A-12856	Sequence 12856, A
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587	60	4.9	390	4	US-09-661-758A-4	Sequence 4, Appli	660	59.5	4.9	1053	4	US-09-328-352-5058	Sequence 5058, Ap
588	60	4.9	390	4	US-09-661-758A-17	Sequence 17, Appl	661	59.5	4.9	1081	3	US-09-369-364A-17	Sequence 17, Appl
589	60	4.9	405	3	US-09-134-001C-4999	Sequence 4999, Ap	662	59.5	4.9	1237	1	US-08-241-853-2	Sequence 2, Appli
590	60	4.9	455	4	US-09-489-039A-12823	Sequence 12823, A	663	59.5	4.9	1237	2	US-08-850-917-2	Sequence 2, Appli
591	60	4.9	462	4	US-09-710-279-906	Sequence 906, App	664	59.5	4.9	1289	2	US-08-542-003-2	Sequence 2, Appli
592	60	4.9	491	3	US-09-134-001C-4612	Sequence 4612, Ap	665	59.5	4.9	1289	2	US-08-322-760A-2	Sequence 2, Appli
593	60	4.9	571	4	US-09-328-352-4633	Sequence 4633, Ap	666	59.5	4.9	1289	4	US-09-236-949-2	Sequence 27, Appl
594	60	4.9	633	4	US-09-248-796A-20407	Sequence 20407, A	667	59.5	4.9	1584	3	US-09-457-040B-27	Sequence 1, Appli
595	60	4.9	744	4	US-09-252-991A-30945	Sequence 30945, A	668	59	4.9	155	2	US-08-801-972-1	Sequence 1, Appli
596	60	4.9	838	4	US-09-894-998A-45	Sequence 45, Appl	669	59	4.9	155	3	US-09-178-881-1	Sequence 1, Appli
597	60	4.9	934	4	US-09-252-991A-19515	Sequence 19515, A	670	59	4.9	225	4	US-09-107-532A-4090	Sequence 4090, Ap
598	60	4.9	1059	4	US-09-489-039A-10044	Sequence 10044, A	671	59	4.9	230	4	US-09-663-600A-92	Sequence 92, Appl
599	60	4.9	1543	4	US-09-904-987-7	Sequence 7, Appli	672	59	4.9	278	4	US-09-270-767-59700	Sequence 59700, A
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602	60	4.9	3144	1	US-08-453-265-6	Sequence 6, Appli	675	59	4.9	292	4	US-09-583-110-4530	Sequence 4530, Ap
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606	60	4.9	3144	4	US-09-538-092-1118	Sequence 1118, Ap	679	59	4.9	310	4	US-09-907-794A-423	Sequence 423, App
607	59.5	4.9	144	4	US-09-107-532A-4029	Sequence 4029, Ap	680	59	4.9	310	4	US-09-905-125A-423	Sequence 423, App
608	59.5	4.9	169	4	US-09-489-039A-8944	Sequence 8944, Ap	681	59	4.9	310	4	US-09-902-775A-423	Sequence 423, App
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693	59	4.9	374	3	US-09-565-538-25	Sequence 25, Appl
694	59	4.9	374	3	US-09-661-468-25	Sequence 25, Appl
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707	59	4.9	505	4	US-09-328-352-4724	Sequence 4, Appli
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713	59	4.9	577	4	US-09-514-245-3	Sequence 3, Appli
714	59	4.9	639	4	US-09-538-092-17	Sequence 17, Appl
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721	59	4.9	1203	4	US-09-909-280A-2	Sequence 2, Appli
722	59	4.9	1236	4	US-08-857-636-60	Sequence 60, Appl
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724	59	4.9	1692	3	US-09-263-933-11	Sequence 11, Appl
725	59	4.9	1692	3	US-09-263-933-18	Sequence 18, Appl
726	59	4.9	1692	4	US-09-919-901-4	Sequence 4, Appli
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731	59	4.9	1692	4	US-10-191-966-18	Sequence 18, Appl
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733	59	4.9	2307	3	US-09-263-933-9	Sequence 9, Appli
734	59	4.9	2307	3	US-09-263-933-16	Sequence 16, Appl
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736	59	4.9	2307	4	US-09-919-901-9	Sequence 9, Appli
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739	59	4.9	2307	4	US-10-191-966-9	Sequence 9, Appli
740	59	4.9	2307	4	US-10-191-966-16	Sequence 16, Appl
741	59	4.9	2307	4	US-09-919-497-70	Sequence 70, Appl
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747	58.5	4.8	142	4	US-09-380-882-9	Sequence 12148, A
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749	58.5	4.8	169	2	US-08-828-832-4	Sequence 46903, A
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754	58.5	4.8	226	1	US-08-505-058-6	Sequence 6, Appli
755	58.5	4.8	226	2	US-08-459-818-26	Sequence 26, Appl
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832	58.5	4.8	2353	3	US-08-913-942-4	Sequence 4, Appli	905	58	4.8	865	4	US-09-608-821-2	Sequence 2, Appli
833	58.5	4.8	2353	3	US-09-669-974-33	Sequence 33, Appli	906	58	4.8	904	4	US-09-252-991A-23202	Sequence 23202, A
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838	58	4.8	125	4	US-09-248-796A-26907	Sequence 26907, A	911	58	4.8	1873	1	US-08-336-257A-7	Sequence 7, Appli
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840	58	4.8	170	4	US-09-107-532A-5197	Sequence 5197, Ap	913	58	4.8	1968	2	US-08-223-305C-45	Sequence 45, Appl
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842	58	4.8	199	3	US-08-737-248-2	Sequence 2, Appli	915	58	4.8	2539	3	US-09-413-814-42	Sequence 42, Appl
843	58	4.8	199	3	US-08-737-248-11	Sequence 11, Appl	916	57.5	4.7	86	4	US-09-621-976-7127	Sequence 7127, Ap
844	58	4.8	213	3	US-08-397-411-12	Sequence 12, Appl	917	57.5	4.7	99	4	US-09-513-999C-4517	Sequence 4517, Ap
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846	58	4.8	225	4	US-09-270-767-55905	Sequence 55905, A	919	57.5	4.7	115	2	US-08-096-762-179	Sequence 179, App
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849	58	4.8	239	2	US-09-213-389-1	Sequence 1, Appli	922	57.5	4.7	122	4	US-09-248-796A-20778	Sequence 20778, A
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852	58	4.8	288	4	US-09-248-796A-16494	Sequence 16494, A	925	57.5	4.7	157	3	US-09-162-021B-10	Sequence 10, Appl
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854	58	4.8	315	4	US-09-270-767-33342	Sequence 33342, A	927	57.5	4.7	178	4	US-09-134-000C-4464	Sequence 4464, Ap
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864	58	4.8	426	4	US-08-311-731A-109	Sequence 109, App	937	57.5	4.7	269	3	US-08-965-056-24	Sequence 24, Appl
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868	58	4.8	448	1	US-08-789-936-5	Sequence 5, Appli	941	57.5	4.7	293	3	US-09-290-333-2	Sequence 2, Appli
869	58	4.8	448	3	US-08-934-254-5	Sequence 5, Appli	942	57.5	4.7	293	4	US-09-782-857A-2	Sequence 2, Appli
870	58	4.8	448	4	US-09-685-775-5	Sequence 5, Appli	943	57.5	4.7	293	4	US-09-879-919-22	Sequence 22, Appl
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872	58	4.8	459	4	US-09-526-309B-1	Sequence 1, Appli	945	57.5	4.7	293	4	US-09-854-864-14	Sequence 14, Appl
873	58	4.8	469	4	US-09-489-039A-9693	Sequence 9693, Ap	946	57.5	4.7	309	3	US-09-422-869-20	Sequence 20, Appl
874	58	4.8	469	4	US-09-252-991A-26991	Sequence 26991, A	947	57.5	4.7	313	4	US-09-489-847-318	Sequence 318, App
875	58	4.8	485	1	US-08-055-797-2	Sequence 2, Appli	948	57.5	4.7	323	3	US-08-706-281A-12	Sequence 12, Appl
876	58	4.8	485	1	US-07-914-284A-7	Sequence 7, Appli	949	57.5	4.7	323	3	US-09-097-231-12	Sequence 12, Appl
877	58	4.8	485	1	US-08-453-956-15	Sequence 15, Appl	950	57.5	4.7	323	4	US-09-353-099-12	Sequence 12, Appl
878	58	4.8	485	1	US-08-086-631-15	Sequence 15, Appl	951	57.5	4.7	339	4	US-09-690-454-66	Sequence 66, Appl
879	58	4.8	485	2	US-08-452-930-15	Sequence 15, Appl	952	57.5	4.7	340	4	US-09-690-454-174	Sequence 174, App
880	58	4.8	485	5	PCT-US93-08174-15	Sequence 15, Appl	953	57.5	4.7	341	4	US-09-366-247-132	Sequence 132, App
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883	58	4.8	486	3	US-08-630-915A-26	Sequence 26, Appl	956	57.5	4.7	431	4	US-09-866-028-83	Sequence 83, Appl
884	58	4.8	486	4	US-09-879-957-26	Sequence 26, Appl	957	57.5	4.7	431	4	US-09-944-457-83	Sequence 83, Appl
885	58	4.8	486	4	US-09-538-092-926	Sequence 926, App	958	57.5	4.7	443	4	US-09-610-906-1	Sequence 1, Appli
886	58	4.8	504	4	US-09-919-497-67	Sequence 67, Appl	959	57.5	4.7	455	1	US-08-035-928-2	Sequence 2, Appl
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888	58	4.8	539	4	US-09-252-991A-33061	Sequence 33061, A	961	57.5	4.7	472	4	US-09-489-039A-8418	Sequence 8418, Ap
889	58	4.8	559	4	US-09-583-110-4273	Sequence 4273, Ap	962	57.5	4.7	482	4	US-09-107-532A-4868	Sequence 4868, Ap
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892	58	4.8	598	4	US-09-198-452A-511	Sequence 511, App	965	57.5	4.7	545	4	US-09-270-767-61684	Sequence 61684, A
893	58	4.8	607	1	US-07-959-943-7	Sequence 7, Appli	966	57.5	4.7	577	6	5310678-3	Patent No. 5310678
894	58	4.8	607	1	US-07-879-617A-12	Sequence 12, Appl	967	57.5	4.7	612	4	US-09-583-110-2911	Sequence 2911, Ap
895	58	4.8	607	1	US-08-753-985-12	Sequence 12, Appl	968	57.5	4.7	658	4	US-09-538-092-1190	Sequence 1190, Ap
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897	58	4.8	633	3	US-09-041-991A-10	Sequence 10, Appl	970	57.5	4.7	693	4	US-10-140-002-406	Sequence 406, App
898	58	4.8	633	4	US-09-608-533A-10	Sequence 10, Appl	971	57.5	4.7	722	4	US-09-252-991A-17407	Sequence 17407, A
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900	58	4.8	651	4	US-09-252-991A-18065	Sequence 18065, A	973	57.5	4.7	771	3	US-09-312-157-8	Sequence 8, Appli
901	58	4.8	653	1	US-07-782-298-2	Sequence 2, Appli	974	57.5	4.7	803	4	US-09-543-681A-4312	Sequence 4312, Ap
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983	57.5	4.7	898	4	US-08-588-189-3	Sequence 3, Appli
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1041	57	4.7	139	2	US-08-485-910-177	Sequence 177, App
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ALIGNMENTS

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; Patent No. 5922566
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; GENERAL INFORMATION:
;   APPLICANT: Bandman, Olga
;   APPLICANT: Golj, Surya K.
;   APPLICANT: Shah, Purvi
;   APPLICANT: Corley, Neil C.
;   TITLE OF INVENTION: NEW TUMOR-ASSOCIATED ANTIGEN
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FASTSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/855,261A
;   FILING DATE: Filed Herewith
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PF-0298 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-0555
;   TELEFAX: 415-845-4166
;   INFORMATION FOR SEQ ID NO: 1:
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;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   LIBRARY: COLNNO719
;   CLONE: 1634851
;   US-08-855-261A-1
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; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: NEW TUMOR-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
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; SOFTWARE: FastSeq for Windows Version 2.0
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; APPLICATION NUMBER: US/09/227,224
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/855,261
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0298 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
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; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNNOT19
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US-09-227-224-1

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OY 178 DSEENKRLIHFSVFLGLLV--GILEVLFGLSQIVIGFLGCLCGVSKRR 225
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DB 143 DRCEAPPRVPMWNTLFSLLVAASCLIEIVLCGIQLVNATIGVFCGDCRKK 192

RESULT 3
US-09-855-288-1
; Sequence 1, Application US/09855288
; Patent No. 6632617
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN
; FILE REFERENCE: PC-0043 CIP
; CURRENT APPLICATION NUMBER: US/09/855,288
; CURRENT FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6632617 1634851CD1
US-09-855-288-1

Query Match 14.0%; Score 170; DB 4; Length 197;
Best Local Similarity 26.5%; Pred. No. 2.8e-11;
Matches 61; Conservative 32; Mismatches 91; Indels 46; Gaps 7;
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OY 3 CCEGWTSCNGFSLVLLLGVLNAIPLIVSLVEEDQFSQNPISCFEWWPPIIGAGLMA 62
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 2 CTGKCARCVGLSLITLCLVCIVANAL-LVPNGETSWTNTNHLSQLVWLMGGFISGLMV 60

OY 63 IPATWSLTARKR-----ACNNRTGMFLSSFFSVITVIGALYCMLSIQALLKPLMCN 117
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 61 LCPGIAAVRAGKGCAGCCGACCGNRCRMLRSVFSSAFGLAIYCLSVSGAGLRNGP----- 116

OY 118 SPSNSNANCEFSLKNISDIHPESFNLQWFENDSCAPPTGFNKPTSNDTMASGWRASSFHF 177
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 117 -----RC-----LMNGEWGYH-----FEDT-AGAYLLNRTLW 142

OY 178 DSEENKRLIHFSVFLGLLV--GILEVLFGLSQIVIGFLGCLCGVSKRR 225
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 143 DRCEAPPRVPMWNTLFSLLVAASCLIEIVLCGIQLVNATIGVFCGDCRKK 192

RESULT 4
US-09-227-357-232
; Sequence 232, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; EARLIER FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
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/ EARLIER FILING DATE: 1997-07-08
/ EARLIER APPLICATION NUMBER: 60/052,803
/ EARLIER FILING DATE: 1997-07-08
/ EARLIER APPLICATION NUMBER: 60/052,732
/ EARLIER FILING DATE: 1997-07-08
/ EARLIER APPLICATION NUMBER: 60/051,931
/ EARLIER FILING DATE: 1997-07-08
/ EARLIER APPLICATION NUMBER: 60/051,932
/ EARLIER FILING DATE: 1997-07-08
/ EARLIER APPLICATION NUMBER: 60/051,916
/ EARLIER FILING DATE: 1997-07-08
/ EARLIER APPLICATION NUMBER: 60/051,930
/ EARLIER FILING DATE: 1997-07-08
/ EARLIER APPLICATION NUMBER: 60/051,918
/ EARLIER FILING DATE: 1997-07-08
/ EARLIER APPLICATION NUMBER: 60/051,920
/ EARLIER FILING DATE: 1997-07-08
/ EARLIER APPLICATION NUMBER: 60/052,733
/ EARLIER FILING DATE: 1997-07-08
/ EARLIER APPLICATION NUMBER: 60/052,795
/ EARLIER FILING DATE: 1997-07-08
/ EARLIER APPLICATION NUMBER: 60/051,919
/ EARLIER FILING DATE: 1997-07-08
/ EARLIER APPLICATION NUMBER: 60/051,928
/ EARLIER FILING DATE: 1997-07-08
/ EARLIER APPLICATION NUMBER: 60/055,722
/ EARLIER FILING DATE: 1997-08-18
/ EARLIER APPLICATION NUMBER: 60/055,723
/ EARLIER FILING DATE: 1997-08-18
/ EARLIER APPLICATION NUMBER: 60/055,948
/ EARLIER FILING DATE: 1997-08-18
/ EARLIER APPLICATION NUMBER: 60/055,949
/ EARLIER FILING DATE: 1997-08-18
/ EARLIER APPLICATION NUMBER: 60/055,953
/ EARLIER FILING DATE: 1997-08-18
/ EARLIER APPLICATION NUMBER: 60/055,950
/ EARLIER FILING DATE: 1997-08-18
/ EARLIER APPLICATION NUMBER: 60/055,947
/ EARLIER FILING DATE: 1997-08-18
/ EARLIER APPLICATION NUMBER: 60/055,964
/ EARLIER FILING DATE: 1997-08-18
/ EARLIER APPLICATION NUMBER: 60/056,360
/ EARLIER FILING DATE: 1997-08-18
/ EARLIER APPLICATION NUMBER: 60/055,684
/ EARLIER FILING DATE: 1997-08-18
/ EARLIER APPLICATION NUMBER: 60/055,984
/ EARLIER FILING DATE: 1997-08-18
/ EARLIER APPLICATION NUMBER: 60/055,954
/ EARLIER FILING DATE: 1997-08-18
/ EARLIER APPLICATION NUMBER: 60/058,785
/ EARLIER FILING DATE: 1997-09-12
/ EARLIER APPLICATION NUMBER: 60/058,664
/ EARLIER FILING DATE: 1997-09-12
/ EARLIER APPLICATION NUMBER: 60/058,660
/ EARLIER FILING DATE: 1997-09-12
/ EARLIER APPLICATION NUMBER: 60/058,661
/ EARLIER FILING DATE: 1997-09-12
/ NUMBER OF SEQ ID NOS: 672
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 232
/ LENGTH: 198
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (198)
/ OTHER INFORMATION: Xaa equals stop translation
US-09-227-357-232
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Query Match          14.0%; Score 170; DB 3; Length 198;
Best Local Similarity 26.5%; Pred. No. 2.8e-11;
Matches 61; Conservative 32; Mismatches 91; Indels 46; Gaps 7;
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QY      3 CCEGWTSCNGFSLVLLLGVLNAIPDIVSLVEEDQFSQNPISCFEWWFPGIIGAGMA 62
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2 CTGKCARCVCGLSLITLCLVCIVANAL-LLPNGETSWTNTNHLSTQVLMGMGFIGGLMV 60
QY      63 IPATWMSLTARKR-----ACCNRRFGMFLSFSSFTVTYIGALYCMILSIOALLKPLMGN 117
        : : : : : : | | | | | | | | | | | | | | | | | | | | | |
Db      61 LCPGIAYVRAGKGCAGCCGACCGNRCRMLRSVFSSAFGVLGAICYLSGAGLRNGP----- 116
QY      118 SPSNSNANCEFSLKNISDIIHPESFNLQWFENDSCAPPTGFNKPSTNDTWASGWRASSFHF 177
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      117 -----RC-----LNGEMGYH-----FEDT-AGAYLLNRTLW 142
QY      178 DSEENKRLIHFSVFLGLLV--GILEVTLFGLSQIVTGFLGCLGVSKRR 225
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      143 DRCEAPRRVVPWNTFLSLVAASCLIEIVLCGIQLVNAVITGVFCGDCRKK 192
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```
RESULT 5
US-08-048-700-2
/ Sequence 2, Application US/08048700
/ Patent No. 5597707
/ GENERAL INFORMATION:
/ APPLICANT: Marken, John
/ APPLICANT: Schieven, Gary L.
/ APPLICANT: Hellstrom, Ingegerd
/ APPLICANT: Hellstrom, Karl E.
/ APPLICANT: Aruffo, Alejandro
/ TITLE OF INVENTION: A Glycoprotein Tumor Associated Antigen
/ TITLE OF INVENTION: Recognized By The Monoclonal Antibody L6, Its
/ TITLE OF INVENTION: Oligonucleotide Sequence and Methods For Their Use
/ Patent No. 5597707
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Bristol-Myers Squibb Company
/ STREET: 3005 First Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98121
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/048,700
/ FILING DATE: 15-APR-1993
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Poor, Brian W.
/ REGISTRATION NUMBER: 32,928
/ REFERENCE/DOCKET NUMBER: ON0089-
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206)728-4800
/ TELEFAX: (206)727-3601
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 202 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ TISSUE TYPE: Colon
/ CELL TYPE: carcinoma
/ CELL LINE: H3347
US-08-048-700-2
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Query Match          14.0%; Score 170; DB 1; Length 202;
Best Local Similarity 27.4%; Pred. No. 2.9e-11;
Matches 62; Conservative 29; Mismatches 77; Indels 58; Gaps 8;
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QY      181  -----ENKRL-THSVFGLLLVGLVLEFGISQIVIGFLGCLG  220
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Db      146  MSECTEKHIVEMNVSFLSTLLALGIEFILLIQIVINGVLGGICG  191

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## RESULT 8

```

US-09-227-224-3
/ Sequence 3, Application US/09227224
/ Patent No. 6350581
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Goli, Surya K.
/ APPLICANT: Shah, Puri
/ APPLICANT: Corley, Neil C.
/ TITLE OF INVENTION: NEW TUMOR-ASSOCIATED ANTIGEN
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/227,224
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/855,261
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0298 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-855-0555
/ TELEFAX: 415-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 202 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 186804
US-09-227-224-3

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Query Match	14.0%;	Score 170;	DB 3;	Length 202;
Best Local Similarity	27.4%;	Pred. No. 2.9e-11;		
Matches 62;	Conservative 29;	Mismatches 77;	Indels 58;	Gaps 8;

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QY      10  CNGFSLVLLLVLLGVLLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAG-LMAIPATMM 68
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      9   CIGHSLVGLALLCIAAN-ILLYFPNGETKYASENHLRFBVWFSSGIVGGGLMLLPAPVF 67
QY      69  SLTARKRAC-----CNNRTGMFLSSFVSIVITVIGALYCMILISIQALLKGPLMCNSPSN 121
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      68  IGLEQDDCCGCCGCHENGCKRCAMLSSTLALLIGAGSGCVIVAALGLAEGPLCLDSLQ- 126
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      122  SNANCEFSLKNISDIHPESFNLQWFENDSCAPPTGFNKPSTNDTMAQWRASSFHFDS- 180
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      127  -----QW-----NYTFAS--TEQYLLDTST 145
QY      181  ----ENKHRL-IHPSVFLGLLVGLILEVFLGLSQIVIGFLGCLCG 220
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      146  WSECTEPKHIVEMVNSLSFSILLATGIEFTLCLIQVINGVLGIGCG 191

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RESULT 9  
US-09-855-288-5

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; Sequence 9, Application US/09855288
; Patent No. 6632617
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN
; FILE REFERENCE: PC-0043 CIP
; CURRENT APPLICATION NUMBER: US/09/855,288
; CURRENT FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PERL Program
; SEQ ID NO 9
; LENGTH: 202
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. 6632617 g186804
US-09-855-288-9

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Query Match	14.0%;	Score 170;	DB 4;	Length 202;
Best Local Similarity	27.4%;	Pred. No. 2.9e-11;		
Matches 62;	Conservative 29;	Mismatches 77;	Indels 58;	Gaps 8;

[illegible]

## RESULT 10

US-08-855-261A-4  
; Sequence 4, Application US/08855261A  
; Patent No. 5922566  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Gold, Surya K.  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: NEW TUMOR-ASSOCIATED ANTIGEN  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/855,261A  
; FILING DATE: Filed Herewith









GenCore version 5.1.6  
OM protein - protein search, using sw model  
Run on: January 24, 2005, 15:52:13 ; Search time 157 Seconds  
(without alignments)  
523.242 Million cell updates/sec

Title: US-10-063-553-48  
Perfect score: 1215  
Sequence: 1 MTCCEGWTSCNGFSHLVLL.....IVIGFLGCLCGVSKRSQIV 229  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2002273 seqs, 358729299 residues  
Total number of hits satisfying chosen parameters: 2002273  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries  
Database : A\_Geneseq\_23Sep04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description

RESULT 1  
ID AAY66703 standard; protein; 229 AA.  
DE Membrane-bound protein PRO994.  
PN WO963088-A2.  
PD 09-DEC-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 3; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 2  
ID AAU29122 standard; protein; 229 AA.  
DE Human PRO polypeptide sequence #99.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 4; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 3  
ID AAB87549 standard; protein; 229 AA.  
DE Human PRO994.  
PN WO200116318-A2.  
PD 08-MAR-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 4; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 4  
ID AAB65226 standard; protein; 229 AA.  
DE Human PRO994 (UNQ518) protein sequence SEQ ID NO:258.  
PN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 4; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 5  
ID ABG95874 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein PRO994.  
PN US2002119130-A1.  
PD 29-AUG-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 5; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 6  
ID ABUS8498 standard; protein; 229 AA.

DE Human PRO polypeptide #99.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 7  
ID ABU88046 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 8  
ID ABU84361 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 9  
ID ABR66235 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 10  
ID ABR65625 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 11  
ID ABU9565 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 12  
ID ABUS8041 standard; protein; 229 AA.  
DE Human PRO polypeptide #73.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 13  
ID ABU59119 standard; protein; 229 AA.  
DE Novel human secreted or transmembrane protein PRO994.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 14  
ID ABU82631 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein PRO994.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 15  
ID ABU82804 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 16  
ID ABU89925 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003036147-A1.

PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 17  
ID ABR68174 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 18  
ID ABU60550 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein, #103.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 19  
ID ABU96227 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 20  
ID ABU92658 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 21  
ID ABO08735 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 22  
ID ABO02787 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 23  
ID ABR74941 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 24  
ID ABR94703 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 25  
ID ABU13932 standard; protein; 229 AA.  
DE Human PRO994 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 26  
ID ABU85676 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003036140-A1.  
PD 20-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 27  
ID ABU98836 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 28  
ID ABU98051 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 29  
ID ABU91757 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 30  
ID ABU89450 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 31  
ID ABU86291 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 32  
ID ABU67504 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 33  
ID ABU80532 standard; protein; 229 AA.  
DE Human PRO protein #99.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 34  
ID ABU72517 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 35  
ID ABU90899 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
PRED. NO. 3.5e-132;  
RESULT 36  
ID ABO33958 standard; protein; 229 AA.

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DE Human secreted/transmembrane protein PRO994.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 37
ID ABR9450 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 38
ID ABR98840 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 39
ID ABO16363 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 40
ID ABR92263 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 41
ID ABO18904 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 42
ID ABR78325 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 43
ID ABU71975 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 44
ID ABU85061 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 45
ID ABO00200 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 46
ID ABO11532 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040060-A1.
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DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 47
ID ABO02177 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 48
ID ABU88751 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 49
ID ABU83446 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 50
ID ABO06247 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 51
ID ABR59283 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 52
ID ABO09345 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 53
ID ABO19209 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 54
ID ABO11227 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 55
ID ABR66845 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 56
ID ABO16058 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040060-A1.
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PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 57
ID ABO13764 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 58
ID ABU71529 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 59
ID ABU65667 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, SEQ ID NO:198.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 60
ID ABO07515 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 61
ID ABO03702 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 62
ID ABR67150 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 63
ID ABO15753 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 64
ID ABU56034 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 65
ID ABU72310 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 66
ID ABU65362 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032102-A1.
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PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 67
ID ABU95307 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 68
ID ABU71210 standard; protein; 229 AA.
DE Human PRO994 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 69
ID ABO07820 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 70
ID ABR70061 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 71
ID ABR69394 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 72
ID ABO01535 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 73
ID ABU81337 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 74
ID ABR60134 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 75
ID ABU90983 standard; protein; 229 AA.
DE Human PRO polypeptide #24.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 76
ID ABR67869 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027269-A1.
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[illegible]

Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	
RESULT 87			
ID ABO93707 standard; protein; 229 AA.			
DE Novel human secreted and transmembrane protein PRO994.			
PN US2003032119-A1.			
PD 13-FEB-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1215;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	Length 229;
RESULT 88			
ID ABO25963 standard; protein; 229 AA.			
DE Human PRO994 polypeptide.			
PN US2002127576-A1.			
PD 12-SEP-2002.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1215;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	Length 229;
RESULT 89			
ID ABR64952 standard; protein; 229 AA.			
DE Human secreted polypeptide PRO994, SEQ ID NO:198.			
PN US2003027263-A1.			
PD 06-FEB-2003.			
Query Match	100.0%;	Score 1215;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	Length 229;
RESULT 90			
ID ABO27304 standard; protein; 229 AA.			
DE Human secreted/transmembrane polypeptide PRO994.			
PN US2003009012-A1.			
PD 09-JAN-2003.			
PA (GETH ) GENENTECH INC.			
Query Match	100.0%;	Score 1215;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	Length 229;
RESULT 91			
ID ABR68784 standard; protein; 229 AA.			
DE Human secreted polypeptide PRO994, SEQ ID NO:198.			
PN US2003027271-A1.			
PD 06-FEB-2003.			
Query Match	100.0%;	Score 1215;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	Length 229;
RESULT 92			
ID ABO06600 standard; protein; 229 AA.			
DE Human secreted/transmembrane protein (PRO) #99.			
PN US2003036125-A1.			
PD 20-FEB-2003.			
Query Match	100.0%;	Score 1215;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	Length 229;
RESULT 93			
ID ABR99145 standard; protein; 229 AA.			
DE Human secreted polypeptide PRO994, SEQ ID NO:198.			
PN US2003040068-A1.			
PD 27-FEB-2003.			
Query Match	100.0%;	Score 1215;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	Length 229;
RESULT 94			
ID ABU57029 standard; protein; 229 AA.			
DE Human PRO polypeptide #99.			
PN US2003027280-A1.			
PD 06-FEB-2003.			
Query Match	100.0%;	Score 1215;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	Length 229;
RESULT 95			
ID ABU85981 standard; protein; 229 AA.			
DE Novel human secreted and transmembrane protein PRO994.			
PN US2003022300-A1.			
PD 30-JAN-2003.			
Query Match	100.0%;	Score 1215;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	Length 229;
RESULT 96			
ID ABU82268 standard; protein; 229 AA.			
DE Novel human secreted and transmembrane protein PRO994.			
PN US2003036136-A1.			
PD 20-FEB-2003.			
Query Match	100.0%;	Score 1215;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	Length 229;
RESULT 97			
ID ABU82268 standard; protein; 229 AA.			
DE Novel human secreted and transmembrane protein PRO994.			
PN US2003036136-A1.			
PD 20-FEB-2003.			
Query Match	100.0%;	Score 1215;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	Length 229;
RESULT 98			
ID ABU82268 standard; protein; 229 AA.			
DE Novel human secreted and transmembrane protein PRO994.			
PN US2003036136-A1.			
PD 20-FEB-2003.			
Query Match	100.0%;	Score 1215;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	Length 229;
RESULT 99			
ID ABU82268 standard; protein; 229 AA.			
DE Novel human secreted and transmembrane protein PRO994.			
PN US2003036136-A1.			
PD 20-FEB-2003.			
Query Match	100.0%;	Score 1215;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	Length 229;
RESULT 100			
ID ABU82268 standard; protein; 229 AA.			
DE Novel human secreted and transmembrane protein PRO994.			
PN US2003036136-A1.			
PD 20-FEB-2003.			
Query Match	100.0%;	Score 1215;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	Length 229;
RESULT 101			
ID ABU82268 standard; protein; 229 AA.			
DE Novel human secreted and transmembrane protein PRO994.			
PN US2003036136-A1.			
PD 20-FEB-2003.			
Query Match	100.0%;	Score 1215;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	Length 229;
RESULT 102			
ID ABU82268 standard; protein; 229 AA.			
DE Novel human secreted and transmembrane protein PRO994.			



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Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 97
ID ABU87279 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 98
ID ABU83751 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 99
ID ABO08125 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 100
ID ABU92499 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 101
ID ABU81836 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 102
ID ABU66000 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 103
ID ABU81169 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 104
ID ABR59829 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 105
ID ABU94017 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 106
ID ABU99870 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 107
ID ABR6540 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 108
ID ABR90958 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 109
ID ABO53284 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 110
ID ABU58972 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, #103.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 111
ID ABU94385 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 112
ID ABU79267 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 113
ID ABU86596 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 114
ID ABU86901 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 115
ID ABU94690 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 116
ID ABO04617 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
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RESULT 117
ID ABR70366 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 118
ID ABU92350 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 119
ID ABU98531 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 120
ID ABR65930 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003036165-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 121
ID ABR64647 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 122
ID ABU59415 standard; protein; 229 AA.
DE Novel human secreted or transmembrane protein PRO812.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 123
ID ABU79572 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 124
ID ABU92963 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 125
ID ABU95922 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 126
ID ABU91142 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 127
ID ABU90235 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 128
ID AB009650 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 129
ID AB010922 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 130
ID ABR70976 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 131
ID ABU98286 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2002183493-A1.
PD 05-DEC-2002.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 132
ID ABU87584 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 133
ID ABU91452 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 134
ID ABU89291 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003036634-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 135
ID ABU84666 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 136
ID ABR69756 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
Pred. No. 3.5e-132;
RESULT 137
ID ABU80133 standard; protein; 229 AA.
DE Human PRO protein #99.
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PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 138  
ID ABU82498 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 139  
ID ABU92181 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 140  
ID ABU93402 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 141  
ID ABO09955 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 142  
ID ABO09040 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 143  
ID ABU96462 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 144  
ID ABU10887 standard; protein; 229 AA.  
DE Human PRO polypeptide #73.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 145  
ID ABU10608 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein #99.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 146  
ID ABU81639 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 147

ID ABU72132 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 148  
ID ABU95617 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 149  
ID ABU96826 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 150  
ID ABR70671 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 151  
ID ABO05022 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 152  
ID ABO08430 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 153  
ID ABU88578 standard; protein; 229 AA.  
DE Human secreted and transmembrane polypeptide PRO994.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 154  
ID ABO34092 standard; protein; 229 AA.  
DE Human PRO994 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 155  
ID ABO05637 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 156  
ID ABR74026 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;  
Pred. No. 3.5e-132;  
RESULT 157

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RESULT 157
ID ABR95618 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 158
ID ABR80915 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 159
ID ABR81220 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 160
ID ABM00916 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 161
ID ABR88518 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 162
ID ABM77339 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 163
ID ABO28823 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 164
ID ABO31568 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 165
ID ABM07985 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 166
ID ABR95618 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 167
ID ABO35890 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 168
ID ABO44029 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 169
ID ADA77950 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 170
ID ABM24824 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 171
ID ABO03092 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 172
ID ABR90348 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 173
ID ABM17262 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 174
ID ABR95008 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 175
ID ABR95313 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
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Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 176  
ID ADB17105 standard; protein; 229 AA.  
DE Human transmembrane PRO polypeptide (SeqID 48) .  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 177  
ID ABO21551 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 178  
ID ABR97815 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 179  
ID ABR87603 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 180  
ID ABM77644 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 181  
ID ABM27874 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 182  
ID ABM06155 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 183  
ID ABM03661 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 184  
ID ABM35112 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 185  
ID ABM26349 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 186  
ID ABO48131 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 187  
ID ABR92873 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 188  
ID ABO24634 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 189  
ID ADA37769 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein PRO994.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 190  
ID ABM11645 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 191  
ID ABM02746 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 192  
ID ABM16042 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 193  
ID ABO27603 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 194



ID ABM29094 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 195  
ID ABM07070 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 196  
ID ABM21164 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 197  
ID ABM09510 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 198  
ID ABO41380 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 199  
ID ABO36195 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 200  
ID ABO43724 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 201  
ID ABM76424 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 202  
ID ABM76120 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 203  
ID ABM25739 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.

PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 204  
ID ABM26044 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 205  
ID ADA21455 standard; protein; 229 AA.  
DE Human secreted/transmembrane polypeptide PRO994.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 206  
ID ABO03397 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 207  
ID ABO02482 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 208  
ID ABO44262 standard; protein; 229 AA.  
DE Human secreted/transmembrane polypeptide PRO 994.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 209  
ID ABR90653 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 210  
ID ABR73721 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 211  
ID ABO16973 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 212  
ID ABR94398 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 213  
ID ABR75905 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.

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PN US2003044929-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 214
ID ABR71281 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 215
ID ABR93178 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 216
ID ABR93483 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 217
ID ADA10242 standard; protein; 229 AA.
DE Human secreted/transmembrane protein, PRO994.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 218
ID ABR87908 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 219
ID ABO27908 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 220
ID ABO30043 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 221
ID ABO33252 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 222
ID ABO04940 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 223
ID ABO08900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 224
ID ABO36500 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 225
ID ABO35585 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 226
ID ABO39550 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 227
ID ABM10425 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 228
ID ABM11950 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 229
ID ABO52096 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 230
ID ABO52401 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 231
ID ADA1910 standard; protein; 229 AA.
DE Novel human secreted and transmembrane protein PRO994.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
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Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 232
ID ABO23719 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 233
ID ADB17293 standard; protein; 229 AA.
DE Human transmembrane PRO polypeptide (SeqID 48) .
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 234
ID ADA17786 standard; protein; 229 AA.
DE Human PRO994 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 235
ID ABR97205 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 236
ID ABR86993 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 237
ID ABM11035 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 238
ID ABM28179 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 239
ID ABO32178 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 240
ID ABM15305 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 241
ID ABM06460 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 242
ID ABM04271 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 243
ID ABM22384 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 244
ID ABM07680 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 245
ID ABO40770 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 246
ID ABM35417 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 247
ID ABM33180 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 248
ID ABO52706 standard; protein; 229 AA.
DE Human PRO polypeptide #99.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 249
ID ABO50266 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 250
ID ABU99260 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040055-A1.
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PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 251
ID ABO04312 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 252
ID ABO05942 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 253
ID ABM18482 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 254
ID ADA27894 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 255
ID ABR97510 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 256
ID ABR80610 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 257
ID ABM01221 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 258
ID ABR88823 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 259
ID ABM13475 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 260
ID ABM20859 standard; protein; 229 AA.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 261
ID ABO41990 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 262
ID ABO42600 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 263
ID ABM10120 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 264
ID ABO38635 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 265
ID ABM32875 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 266
ID ABM22689 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 267
ID ABM74900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 268
ID ADA79742 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
RESULT 269
ID ABR96290 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1215; DB 6; Length 229;
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Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 270  
ID ABM02441 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003059886-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 271  
ID ABR86383 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 272  
ID ABR86688 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 273  
ID ABM16652 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 274  
ID ABM29704 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 275  
ID ABO29128 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068693-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 276  
ID ABM23909 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 277  
ID ABM23299 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 278  
ID ABM22079 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 279  
ID ABO37720 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 280  
ID ABM28484 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 281  
ID ABM28789 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 282  
ID ABM66433 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 283  
ID ABM75815 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 284  
ID ABM34095 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 285  
ID ABM34400 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 286  
ID ABO20331 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 287  
ID ABO21246 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 288  
ID ABO22161 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003054477-A1.  
PD 20-MAR-2003.



PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 289  
ID ADA20082 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 290  
ID ABO34190 standard; protein; 229 AA.  
DE Human secreted/transmembrane polypeptide PRO 994.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 291  
ID ABR96595 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 292  
ID ADA94474 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein PRO994.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 293  
ID ABR85773 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 294  
ID ABR99755 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 295  
ID ABM00306 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 296  
ID ABM00611 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003073172-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 297  
ID ABO29738 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 298

ID ABM23604 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 299  
ID ABM29399 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 300  
ID ABO38330 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 301  
ID ABO45630 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 302  
ID ABM20554 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 303  
ID ADA81469 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 304  
ID ABO16668 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 305  
ID ABO18294 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 306  
ID ABO22721 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 307  
ID ABO23026 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003054461-A1.  
PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 308  
ID ABR92568 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 309  
ID ABR81525 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 310  
ID ABM77949 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 311  
ID ABR89738 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 312  
ID ABM26654 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 313  
ID ABM13780 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 314  
ID ABO28518 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 315  
ID ABO30348 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 316  
ID ABM07375 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 317  
ID ABM03966 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 318  
ID ABO37110 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 319  
ID ABO41685 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 320  
ID ABO35280 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 321  
ID ABM25129 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 322  
ID ABO47521 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 323  
ID ABO47826 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 324  
ID ABO48436 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 325  
ID ABO51486 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 326  
ID ABO51791 standard; protein; 229 AA.

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DE Human PRO polypeptide #99.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 327
ID ABO50571 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 328
ID ABR79695 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 329
ID ABM16957 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003040078-A1.
PD 27-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 330
ID ABO17989 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 331
ID ABO20941 standard; protein; 229 AA.
DE Human secreted/transmembrane protein (PRO) #99.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 332
ID ABR96900 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 333
ID ADA38699 standard; protein; 229 AA.
DE Human secreted/transmembrane protein PRO994.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 334
ID ABM12255 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
RESULT 335
ID ABM16347 standard; protein; 229 AA.
DE Human secreted polypeptide PRO994, SEQ ID NO:198.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1215; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.5e-132;
Query Match      100.0%; Score 1215; DB 6; Length 229;
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Best Local Similarity	100.0%;	Pred. No. 3.5e-132;	
RESULT 336			
ID	ABM24214 standard; protein; 229 AA.		
DE	Human secreted polypeptide PRO994, SEQ ID NO:198.		
PN	US2003064441-A1.		
PD	03-APR-2003.		
Query Match			
Best Local Similarity	100.0%;	Score 1215; DB 6;	Length 229;
RESULT 337			
ID	ABM14695 standard; protein; 229 AA.		
DE	Human secreted polypeptide PRO994, SEQ ID NO:198.		
PN	US2003068696-A1.		
PD	10-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match			
Best Local Similarity	100.0%;	Score 1215; DB 6;	Length 229;
RESULT 338			
ID	ABM04576 standard; protein; 229 AA.		
DE	Human secreted polypeptide PRO994, SEQ ID NO:198.		
PN	US2003068712-A1.		
PD	10-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match			
Best Local Similarity	100.0%;	Score 1215; DB 6;	Length 229;
RESULT 339			
ID	ABM06765 standard; protein; 229 AA.		
DE	Human secreted polypeptide PRO994, SEQ ID NO:198.		
PN	US2003068730-A1.		
PD	10-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match			
Best Local Similarity	100.0%;	Score 1215; DB 6;	Length 229;
RESULT 340			
ID	ABM09205 standard; protein; 229 AA.		
DE	Human secreted polypeptide PRO994, SEQ ID NO:198.		
PN	US2003073174-A1.		
PD	17-APR-2003.		
Query Match			
Best Local Similarity	100.0%;	Score 1215; DB 6;	Length 229;
RESULT 341			
ID	ABO39245 standard; protein; 229 AA.		
DE	Human secreted/transmembrane protein (PRO) #99.		
PN	US2003068775-A1.		
PD	10-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match			
Best Local Similarity	100.0%;	Score 1215; DB 6;	Length 229;
RESULT 342			
ID	ABM75510 standard; protein; 229 AA.		
DE	Human secreted polypeptide PRO994, SEQ ID NO:198.		
PN	US2003104545-A1.		
PD	05-JUN-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match			
Best Local Similarity	100.0%;	Score 1215; DB 6;	Length 229;
RESULT 343			
ID	ABM25434 standard; protein; 229 AA.		
DE	Human secreted polypeptide PRO994, SEQ ID NO:198.		
PN	US2003104541-A1.		
PD	05-JUN-2003.		
Query Match			
Best Local Similarity	100.0%;	Score 1215; DB 6;	Length 229;
RESULT 344			
ID	ABM19944 standard; protein; 229 AA.		
DE	Human secreted polypeptide PRO994, SEQ ID NO:198.		
PN	US2003104554-A1.		
PD	05-JUN-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match			
Best Local Similarity	100.0%;	Score 1215; DB 6;	Length 229;
RESULT 345			
ID	ABO46850 standard; protein; 229 AA.		
DE	Human PRO polypeptide #99.		

PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 346  
ID ABO47155 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 347  
ID ADA83267 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 348  
ID ABR71586 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 349  
ID ABR72196 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 350  
ID ABR98535 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 351  
ID ABO06905 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 352  
ID ABR84858 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 353  
ID ABR73416 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 354  
ID ABR76510 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 355  
ID ABR73111 standard; protein; 229 AA.

DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 356  
ID ABM18177 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 357  
ID ABO20636 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 358  
ID ABO25379 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 359  
ID ABO25684 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 360  
ID ABR94093 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 361  
ID ADA92820 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein PRO994.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 362  
ID ABR80000 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 363  
ID ABM11340 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 364  
ID ABO32947 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;

Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 365  
ID ABO30653 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 366  
ID ABO30958 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 367  
ID ABM27264 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 368  
ID ABM30009 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 369  
ID ABM05545 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 370  
ID ABM15610 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 371  
ID ABM08595 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 372  
ID ABO42295 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 373  
ID ABO38025 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 374  
ID ABO45935 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 375  
ID ABM66738 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 376  
ID ADB20310 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 377  
ID ABM19639 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 378  
ID ABO49351 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 379  
ID ABO49656 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 380  
ID ADA78562 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 381  
ID ABR88213 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 382  
ID ADA00379 standard; protein; 229 AA.  
DE Human secreted/transmembrane polypeptide PRO 994.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 383  
ID ABM26959 standard; protein; 229 AA.

Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 383  
ID ABM26959 standard; protein; 229 AA.



DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 384  
ID ABM03356 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 385  
ID ABO39855 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 6; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 386  
ID ABO49961 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 387  
ID ABO50876 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 388  
ID ABO05332 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 389  
ID ABR74636 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 390  
ID ABR77115 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 391  
ID ABM17872 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 392  
ID ABR95923 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 393  
ID ABO34975 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.

RESULT 393  
ID ABO21856 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 394  
ID ABO20026 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 395  
ID ABO24329 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 396  
ID ABR86078 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 397  
ID ABM10730 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 398  
ID ABM76729 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 399  
ID ABR89433 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003073170-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 400  
ID ABM12560 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 401  
ID ABM05850 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 402  
ID ABO34975 standard; protein; 229 AA.

PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 403  
ID ABM03051 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 404  
ID ABM19029 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 405  
ID ABM19334 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 406  
ID ABO46545 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 407  
ID ABO49046 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 408  
ID ABR69089 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 409  
ID ABR89128 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 410  
ID ABR72501 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 411  
ID ABR74331 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 412

Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 412  
ID ABO18599 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 413  
ID ABR80305 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 414  
ID ABM01526 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 415  
ID ABM02136 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 416  
ID ABR87298 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 417  
ID ABR12865 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 418  
ID ABM30619 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 419  
ID ABM24519 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 420  
ID ABO29433 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 421

ID ABO31263 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 422  
ID ABM14390 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 423  
ID ABM09815 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 424  
ID ABO38940 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 425  
ID ABM34705 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 426  
ID ABO51181 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 427  
ID ABO04007 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 428  
ID ABO10477 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 429  
ID ABO53178 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein PRO994.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 430  
ID ABR77720 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;

Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 431  
ID ABR78930 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 432  
ID ABO24024 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 433  
ID ABR93788 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 434  
ID ABM01831 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 435  
ID ABM78254 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 436  
ID ABR90043 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 437  
ID ADA22381 standard; protein; 229 AA.  
DE Human secreted/transmembrane polypeptide PRO994.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 438  
ID ABM27569 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 439  
ID ABM13170 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 440  
ID ABO31873 standard; protein; 229 AA.

DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 441  
ID ABO14085 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 442  
ID ABO08290 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 443  
ID ABO40160 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 444  
ID ABO74595 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 445  
ID ABO33790 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 446  
ID ABO20249 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 447  
ID ABO48741 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 448  
ID ABO22548 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein PRO994.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 449  
ID ABR72806 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;

Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 450  
ID ABO15448 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 451  
ID ABR85163 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 452  
ID ABO15143 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 453  
ID ABO17278 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 454  
ID ABR17567 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 455  
ID ADA06547 standard; protein; 229 AA.  
DE Human secreted/transmembrane PRO polypeptide #73.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 456  
ID ADA39240 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein PRO994.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 457  
ID ABR85468 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 458  
ID ABO77034 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 459  
ID ABO28213 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 460  
ID ABM22994 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 461  
ID ABM30314 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 462  
ID ABM21774 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 463  
ID ABM21469 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 464  
ID ABM15000 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 465  
ID ABO41075 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 466  
ID ABO36805 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 467  
ID ABO37415 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 468  
ID ABM75205 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 469  
ID ABM32449 standard; protein; 229 AA.

Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 469  
ID ABM33485 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 470  
ID ABO46240 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 471  
ID ADA82633 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 472  
ID ADB85621 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 473  
ID ADB96266 standard; protein; 229 AA.  
DE Human PRO polypeptide #73.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 474  
ID ADB31839 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 475  
ID ABM31229 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 476  
ID ADB85941 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein (PRO) #99.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 477  
ID ABM32144 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 478  
ID ABM32449 standard; protein; 229 AA.



DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 479  
ID ADB68300 standard; protein; 229 AA.  
DE Human PRO994 protein.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 480  
ID ADB68107 standard; protein; 229 AA.  
DE Human PRO994 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 481  
ID ABM31534 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 482  
ID ABM30924 standard; protein; 229 AA.  
DE Human secreted polypeptide PRO994, SEQ ID NO:198.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 483  
ID ADB90924 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 484  
ID ADC57738 standard; protein; 229 AA.  
DE Human PRO polypeptide #73.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 485  
ID ADC55102 standard; protein; 229 AA.  
DE Human PRO polypeptide #73.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 486  
ID ADC11969 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein PRO994.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 487  
ID ADC07004 standard; protein; 229 AA.  
DE Human PRO994 protein.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 488  
ID ADC56391 standard; protein; 229 AA.  
DE Human PRO polypeptide #73.  
PN US2003064375-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 489  
ID ADC17183 standard; protein; 229 AA.  
DE Mammalian PRO polypeptide (SeqId 48).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 490  
ID ADC07446 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein PRO994.  
PN US2003068647-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 491  
ID ADC11436 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein PRO994.  
PN US2003069403-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 492  
ID ADC14881 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 493  
ID ADC52376 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003138882-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 494  
ID ADC14558 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 495  
ID ADD08090 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003068623-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 496  
ID ADC81915 standard; protein; 229 AA.  
DE Human PRO polypeptide #73.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 497  
ID ADD07557 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2002193299-A1.  
PD 19-DEC-2002.

[illegible]

Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 517  
ID ADH24080 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 518  
ID ADH34106 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 519  
ID ADH29939 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 520  
ID ADH23910 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 521  
ID ADH09023 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 522  
ID ADG85314 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 523  
ID ADH24590 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 524  
ID ADH37446 standard; protein; 229 AA.  
DE Human secreted and transmembrane protein PRO994.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 525  
ID ADH02035 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 526  
ID ADH37616 standard; protein; 229 AA.  
DE Human secreted and transmembrane protein PRO994.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 527  
ID ADG85654 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 528  
ID ADH24250 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 529  
ID ADH38544 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 530  
ID ADG83665 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 531  
ID ADH29473 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 532  
ID ADH27589 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 533  
ID ADH37786 standard; protein; 229 AA.  
DE Human secreted and transmembrane protein PRO994.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 534  
ID ADH37963 standard; protein; 229 AA.  
DE Human secreted and transmembrane protein PRO994.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

ID ADH57383 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 536  
ID ADH53525 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 537  
ID ADH53695 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 538  
ID ADH52031 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 539  
ID ADH49886 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 540  
ID ADI25396 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 541  
ID ADH90189 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 542  
ID ADI25566 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 543  
ID ADH97740 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 544  
ID ADI35439 standard; protein; 229 AA.

DE Human PRO polypeptide #73.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 545  
ID ADI03588 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 546  
ID ADI11945 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 547  
ID ADH90019 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 548  
ID ADH99931 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 549  
ID ADH98420 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 550  
ID ADI11095 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 551  
ID ADI11605 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 552  
ID ADH98250 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 553  
ID ADH98590 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181708-A1.  
PD 25-SEP-2003.

PA	(GETH ) GENENTECH INC.	100.0%;	Score 1215;	DB 7;	Length 229;
Query Match					
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;			
RESULT 554					
ID	ADH98080 standard; protein; 229 AA.				
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003181673-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 1215;	DB 7;	Length 229;	
RESULT 555					
ID	AD105068 standard; protein; 229 AA.				
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003180848-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 1215;	DB 7;	Length 229;	
RESULT 556					
ID	AD103418 standard; protein; 229 AA.				
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003181654-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 1215;	DB 7;	Length 229;	
RESULT 557					
ID	AD104813 standard; protein; 229 AA.				
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003181657-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 1215;	DB 7;	Length 229;	
RESULT 558					
ID	ADH78267 standard; protein; 229 AA.				
DE	Human PRO polypeptide #24.				
PN	US2003181668-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 1215;	DB 7;	Length 229;	
RESULT 559					
ID	AD119611 standard; protein; 229 AA.				
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003181676-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 1215;	DB 7;	Length 229;	
RESULT 560					
ID	ADH90359 standard; protein; 229 AA.				
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003181699-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 1215;	DB 7;	Length 229;	
RESULT 561					
ID	AD103078 standard; protein; 229 AA.				
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003181653-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 1215;	DB 7;	Length 229;	
RESULT 562					
ID	ADH77927 standard; protein; 229 AA.				
DE	Human PRO polypeptide #24.				
PN	US2003181666-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 1215;	DB 7;	Length 229;	
RESULT 563					
ID	ADH97910 standard; protein; 229 AA.				
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003181674-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 1215;	DB 7;	Length 229;	
RESULT 564					
ID	AD101295 standard; protein; 229 AA.				
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003190669-A1.				
PD	09-OCT-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					
Best Local Similarity	100.0%;	Score 1215;	DB 7;	Length 229;	
RESULT 565					
ID	AD101990 standard; protein; 229 AA.				
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003181652-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match					</



Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 572  
ID ADI19441 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 573  
ID ADI05242 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 574  
ID ADH79654 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 575  
ID ADI01480 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 576  
ID ADI01650 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 577  
ID ADI01820 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 578  
ID ADH79824 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 579  
ID ADI04642 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 580  
ID ADI02778 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 581  
ID ADH78097 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 582  
ID ADI25736 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 583  
ID ADI25906 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 584  
ID ADK65418 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 585  
ID ADH98760 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 586  
ID ADH80001 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 587  
ID ADL32804 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 588  
ID ADM30338 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 589  
ID ADL93732 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 7; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 590

ID	ADG52186	standard; protein; 229 AA.			
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003130483-A1.				
PD	10-JUL-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1215;	DB 8;	Length 229
Best Local Similarity		100.0%;	Pred. No. 3.5e-132;		
RESULT 591					
ID	ADE74335	standard; protein; 229 AA.			
DE	Human secreted/transmembrane protein (PRO) #99.				
PN	US2003211572-A1.				
PD	13-NOV-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1215;	DB 8;	Length 229
Best Local Similarity		100.0%;	Pred. No. 3.5e-132;		
RESULT 592					
ID	ADE74947	standard; protein; 229 AA.			
DE	Human secreted/transmembrane protein (PRO) #99.				
PN	US2003211574-A1.				
PD	13-NOV-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1215;	DB 8;	Length 229
Best Local Similarity		100.0%;	Pred. No. 3.5e-132;		
RESULT 593					
ID	ADF35384	standard; protein; 229 AA.			
DE	Human PRO994 polypeptide.				
PN	US2003194760-A1.				
PD	16-OCT-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1215;	DB 8;	Length 229
Best Local Similarity		100.0%;	Pred. No. 3.5e-132;		
RESULT 594					
ID	ADG11634	standard; protein; 229 AA.			
DE	Human PRO994 polypeptide.				
PN	US2003228655-A1.				
PD	11-DEC-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1215;	DB 8;	Length 229
Best Local Similarity		100.0%;	Pred. No. 3.5e-132;		
RESULT 595					
ID	ADF96160	standard; protein; 229 AA.			
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003215909-A1.				
PD	20-NOV-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1215;	DB 8;	Length 229
Best Local Similarity		100.0%;	Pred. No. 3.5e-132;		
RESULT 596					
ID	ADG04431	standard; protein; 229 AA.			
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003215912-A1.				
PD	20-NOV-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1215;	DB 8;	Length 229
Best Local Similarity		100.0%;	Pred. No. 3.5e-132;		
RESULT 597					
ID	ADG00591	standard; protein; 229 AA.			
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003215911-A1.				
PD	20-NOV-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1215;	DB 8;	Length 229
Best Local Similarity		100.0%;	Pred. No. 3.5e-132;		
RESULT 598					
ID	ADH06618	standard; protein; 229 AA.			
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003180852-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1215;	DB 8;	Length 229
Best Local Similarity		100.0%;	Pred. No. 3.5e-132;		
RESULT 599					
ID	ADH06448	standard; protein; 229 AA.			
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003180853-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				
Query Match		100.0%;	Score 1215;	DB 8;	Length 229
Best Local Similarity		100.0%;	Pred. No. 3.5e-132;		
RESULT 599					
ID	ADH06448	standard; protein; 229 AA.			
DE	Novel human secreted and transmembrane protein PRO994.				
PN	US2003180853-A1.				
PD	25-SEP-2003.				
PA	(GETH ) GENENTECH INC.				

Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 600				
ID ADG68869 standard; protein; 229 AA.				
DE Novel human secreted and transmembrane protein PRO994.				
PN US2003180855-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 601				
ID ADH27759 standard; protein; 229 AA.				
DE Novel human secreted and transmembrane protein PRO994.				
PN US2003180912-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 602				
ID ADH25100 standard; protein; 229 AA.				
DE Novel human secreted and transmembrane protein PRO994.				
PN US2003180913-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 603				
ID ADH33732 standard; protein; 229 AA.				
DE Human PRO polypeptide #24.				
PN US2003181645-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 604				
ID ADG82847 standard; protein; 229 AA.				
DE Human PRO polypeptide #99.				
PN US2003215910-A1.				
PD 20-NOV-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 605				
ID ADH02375 standard; protein; 229 AA.				
DE Human PRO polypeptide #24.				
PN US2003180839-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 606				
ID ADH07982 standard; protein; 229 AA.				
DE Novel human secreted and transmembrane protein PRO994.				
PN US2003180845-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 607				
ID ADG69379 standard; protein; 229 AA.				
DE Novel human secreted and transmembrane protein PRO994.				
PN US2003180846-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 608				
ID ADH39200 standard; protein; 229 AA.				
DE Novel human secreted and transmembrane protein PRO994.				
PN US2003180917-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 609				
ID ADH39200 standard; protein; 229 AA.				
DE Novel human secreted and transmembrane protein PRO994.				
PN US2003180917-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 610				
ID ADH39200 standard; protein; 229 AA.				
DE Novel human secreted and transmembrane protein PRO994.				
PN US2003180917-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 611				
ID ADH39200 standard; protein; 229 AA.				
DE Novel human secreted and transmembrane protein PRO994.				
PN US2003180917-A1.				
PD 25-SEP-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1215;	DB 8;	Length 229;
Best Local Similarity	100.0%;	Pred. No. 3.5e-132;		
RESULT 612				
ID ADH39200 standard; protein; 229 AA.				
DE Novel human secreted and transmembrane protein PRO994.				
PN US2003180917-A1.				
PD 25-SEP-2003.				

Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 609  
ID ADH26128 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 610  
ID ADG83940 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 611  
ID ADH19504 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein PRO994.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 612  
ID ADG85484 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 613  
ID ADH06278 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 614  
ID ADH30108 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 615  
ID ADH24420 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 616  
ID ADH33097 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 617  
ID ADG69549 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;

RESULT 618  
ID ADH07812 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 619  
ID ADG85824 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 620  
ID ADH39370 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 621  
ID ADH33562 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 622  
ID ADH33902 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 623  
ID ADH01112 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 624  
ID ADG69719 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 625  
ID ADH20997 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein PRO994.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 626  
ID ADH02205 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 627  
ID ADG69209 standard; protein; 229 AA.

DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 628  
ID ADG85994 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 629  
ID ADH24930 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 630  
ID ADH39547 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 631  
ID ADH20037 standard; protein; 229 AA.  
DE Human secreted/transmembrane protein PRO994.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 632  
ID ADH02545 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 633  
ID ADG69039 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 634  
ID ADH07642 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 635  
ID ADG86164 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 636  
ID ADH24760 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.

PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 637  
ID ADH25808 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 638  
ID ADH38374 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 639  
ID ADH57213 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 640  
ID ADH52201 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 641  
ID ADH49567 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 642  
ID ADH90529 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 643  
ID ADI11265 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 644  
ID ADH98930 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 645  
ID ADI02160 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003190699-A1.

PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 646  
ID ADH90699 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 647  
ID ADJ54836 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 648  
ID ADJ98574 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 649  
ID ADJ98744 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 650  
ID ADH78903 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 651  
ID ADJ99137 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 652  
ID ADJ99307 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 653  
ID ADJ98925 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 654  
ID ADH79073 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003181702-A1.  
PD 25-SEP-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 655  
ID ADK00933 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 656  
ID ADK14454 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 657  
ID ADJ64607 standard; protein; 229 AA.  
DE Human PRO polypeptide #99.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 658  
ID ADM31503 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 659  
ID ADM36550 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 660  
ID ADM40355 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 661  
ID ADM80903 standard; protein; 229 AA.  
DE Human PRO polypeptide #24.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 662  
ID ADN37963 standard; protein; 229 AA.  
DE Novel human secreted and transmembrane protein PRO994.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1215; DB 8; Length 229;  
Best Local Similarity 100.0%; Pred. No. 3.5e-132;  
RESULT 663  
ID ABP41230 standard; protein; 205 AA.  
DE Human ovarian antigen HSPS174, SEQ ID NO:2362.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.



Query Match 14.3%; Score 173.5; DB 5; Length 205;  
Best Local Similarity 27.7%; Pred. No. 3e-11;  
RESULT 664  
ID AAW61625 standard; protein; 197 AA.  
DE Clone HGBGV89 of TM4SF superfamily.  
PN WO9831799-A2.  
PD 23-JUL-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 14.0%; Score 170; DB 2; Length 197;  
Best Local Similarity 26.5%; Pred. No. 7.2e-11;  
RESULT 665  
ID AAW88494 standard; protein; 197 AA.  
DE Human stomach cancer clone HP01440-encoded transmembrane protein.  
PN WO9855508-A2.  
PD 10-DEC-1998.  
PA (SAGA ) SAGAMI CHEM RES CENTRE.  
PA (PROT-) PROTEGENE INC.  
Query Match 14.0%; Score 170; DB 2; Length 197;  
Best Local Similarity 26.5%; Pred. No. 7.2e-11;  
RESULT 666  
ID AAW84273 standard; protein; 197 AA.  
DE A tumour associated antigen designated TUAN.  
PN WO9851706-A1.  
PD 19-NOV-1998.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 14.0%; Score 170; DB 2; Length 197;  
Best Local Similarity 26.5%; Pred. No. 7.2e-11;  
RESULT 667  
ID ADD10280 standard; protein; 197 AA.  
DE Human tumour-associated antigen, TUAN.  
PN US632617-B1.  
PD 14-OCT-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 14.0%; Score 170; DB 7; Length 197;  
Best Local Similarity 26.5%; Pred. No. 7.2e-11;  
RESULT 668  
ID ABW01507 standard; protein; 197 AA.  
DE Human receptor protein from clone HGBGV89.  
PN US2003129696-A1.  
PD 10-JUL-2003.  
PA (NIJ/) NI J.  
PA (ROSE/) ROSEN C A.  
PA (GENT/) GENTZ R.  
Query Match 14.0%; Score 170; DB 7; Length 197;  
Best Local Similarity 26.5%; Pred. No. 7.2e-11;  
RESULT 669  
ID ADN41032 standard; protein; 197 AA.  
DE Novel human secreted protein seqid 154.  
PN US2004044191-A1.  
PD 04-MAR-2004.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAF/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHI/) SHI Y.  
PA (OLSE/) OLSEN H.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
Query Match 14.0%; Score 170; DB 8; Length 197;  
Best Local Similarity 26.5%; Pred. No. 7.2e-11;  
RESULT 670  
ID AAY02732 standard; protein; 198 AA.  
DE Human secreted protein encoded by gene 83 clone HGBGV89.  
PN WO9902546-A1.  
PD 21-JAN-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 14.0%; Score 170; DB 2; Length 198;  
Best Local Similarity 26.5%; Pred. No. 7.3e-11;

RESULT 671  
ID ADA07411 standard; protein; 198 AA.  
DE Human secreted protein from gene 83.  
PN US2003064412-A1.  
PD 03-APR-2003.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAF/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHI/) SHI Y.  
PA (OLSE/) OLSEN H S.  
PA (EBNE/) EBNER R.  
PA (BREW/) BREWER L A.  
Query Match 14.0%; Score 170; DB 7; Length 198;  
Best Local Similarity 26.5%; Pred. No. 7.3e-11;  
RESULT 672  
ID AAW14123 standard; protein; 202 AA.  
DE Human tumour-associated L6 antigen.  
PN US5597707-A.  
PD 28-JAN-1997.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 14.0%; Score 170; DB 2; Length 202;  
Best Local Similarity 27.4%; Pred. No. 7.5e-11;  
RESULT 673  
ID AAY92049 standard; protein; 202 AA.  
DE HRPca3 polypeptide from androgen-inducible gene clone.  
PN WO200018961-A2.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 14.0%; Score 170; DB 3; Length 202;  
Best Local Similarity 27.4%; Pred. No. 7.5e-11;  
RESULT 674  
ID AAB34199 standard; protein; 202 AA.  
DE Gene 36 human secreted protein homologous amino acid sequence #167.  
PN WO200056755-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 14.0%; Score 170; DB 3; Length 202;  
Best Local Similarity 27.4%; Pred. No. 7.5e-11;  
RESULT 675  
ID ABP68619 standard; protein; 202 AA.  
DE Human pancreatic cancer expressed protein SEQ ID NO 168.  
PN WO200260317-A2.  
PD 08-AUG-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 14.0%; Score 170; DB 5; Length 202;  
Best Local Similarity 27.4%; Pred. No. 7.5e-11;  
RESULT 676  
ID ADD10288 standard; protein; 202 AA.  
DE human tumour-associated L6antigen.  
PN US632617-B1.  
PD 14-OCT-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 14.0%; Score 170; DB 7; Length 202;  
Best Local Similarity 27.4%; Pred. No. 7.5e-11;  
RESULT 677  
ID ABW01521 standard; protein; 202 AA.  
DE Protein #9 used in the present invention.  
PN US2003129696-A1.  
PD 10-JUL-2003.  
PA (NIJ/) NI J.  
PA (ROSE/) ROSEN C A.  
PA (GENT/) GENTZ R.  
Query Match 14.0%; Score 170; DB 7; Length 202;  
Best Local Similarity 27.4%; Pred. No. 7.5e-11;  
RESULT 678  
ID ADF61842 standard; protein; 202 AA.  
DE Human transmembrane 4 superfamily member 1 protein.

PN WO2003088910-A2.  
PD 30-OCT-2003.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match 14.0%; Score 170; DB 7; Length 202;  
Best Local Similarity 27.4%; Pred. No. 7.5e-11;  
RESULT 679  
ID ADK98674 standard; protein; 202 AA.  
DE Human prostate cancer associated protein HRPca 3.  
PN US2003138865-A1.  
PD 24-JUL-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 14.0%; Score 170; DB 7; Length 202;  
Best Local Similarity 27.4%; Pred. No. 7.5e-11;  
RESULT 680  
ID ADN40006 standard; protein; 202 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C376.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 14.0%; Score 170; DB 7; Length 202;  
Best Local Similarity 27.4%; Pred. No. 7.5e-11;  
RESULT 681  
ID ABP68635 standard; protein; 202 AA.  
DE Human pancreatic cancer expressed protein SEQ ID NO 4558.  
PN WO200260317-A2.  
PD 08-AUG-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 13.7%; Score 166.5; DB 5; Length 202;  
Best Local Similarity 26.7%; Pred. No. 1.9e-10;  
RESULT 682  
ID ADN39985 standard; protein; 202 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C355.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 13.7%; Score 166.5; DB 7; Length 202;  
Best Local Similarity 26.7%; Pred. No. 1.9e-10;  
RESULT 683  
ID ADI21569 standard; protein; 209 AA.  
DE Novel human polypeptide #48.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.7%; Score 166.5; DB 7; Length 209;  
Best Local Similarity 26.7%; Pred. No. 2e-10;  
RESULT 684  
ID ABW01520 standard; protein; 197 AA.  
DE Protein #8 used in the present invention.  
PN US2003129696-A1.  
PD 10-JUL-2003.  
PA (NIJ/) NI J.  
PA (ROSE/) ROSEN C A.  
PA (GENT/) GENTZ R.  
Query Match 13.7%; Score 166; DB 7; Length 197;  
Best Local Similarity 26.1%; Pred. No. 2.1e-10;  
RESULT 685  
ID ABR61633 standard; protein; 202 AA.  
DE LRTM4 protein #SEQ ID 2.  
PN CN1367179-A.  
PD 04-SEP-2002.  
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.  
Query Match 13.2%; Score 160.5; DB 6; Length 202;  
Best Local Similarity 21.6%; Pred. No. 9.5e-10;  
RESULT 686  
ID ADD10289 standard; protein; 202 AA.  
DE Mouse tumour-associated ligand.  
PN US6632617-B1.  
PD 14-OCT-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 13.2%; Score 160; DB 7; Length 202;  
Best Local Similarity 23.6%; Pred. No. 1.1e-09;  
RESULT 687  
ID AAO30178 standard; protein; 132 AA.

DE Human transmembrane 4 super family member 5 splice variant (TM4SF5).  
PN WO2003046180-A2.  
PD 05-JUN-2003.  
PA (GEST) GENSET SA.  
Query Match 12.6%; Score 153; DB 6; Length 132;  
Best Local Similarity 34.5%; Pred. No. 3.9e-09;  
RESULT 688  
ID ADI21083 standard; protein; 184 AA.  
DE Novel human protein #58.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.1%; Score 147.5; DB 7; Length 184;  
Best Local Similarity 25.2%; Pred. No. 2.7e-08;  
RESULT 689  
ID AAB44087 standard; protein; 153 AA.  
DE Human cancer associated protein sequence SEQ ID NO:1532.  
PN WO200055350-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.9%; Score 144; DB 3; Length 153;  
Best Local Similarity 33.3%; Pred. No. 5.3e-08;  
RESULT 690  
ID AAB54023 standard; protein; 245 AA.  
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:475.  
PN WO200055320-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 11.7%; Score 142; DB 3; Length 245;  
Best Local Similarity 31.0%; Pred. No. 1.8e-07;  
RESULT 691  
ID ABB72399 standard; protein; 145 AA.  
DE Human protein isolated from skin cells SEQ ID NO: 723.  
PN WO200190357-A1.  
PD 29-NOV-2001.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 11.6%; Score 140.5; DB 5; Length 145;  
Best Local Similarity 33.3%; Pred. No. 1.3e-07;  
RESULT 692  
ID ADD69578 standard; protein; 170 AA.  
DE Human REMAP protein - SEQ ID 7.  
PN WO2003048305-A2.  
PD 12-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 11.4%; Score 138.5; DB 7; Length 170;  
Best Local Similarity 24.9%; Pred. No. 2.7e-07;  
RESULT 693  
ID AAW61626 standard; protein; 201 AA.  
DE Clone HUVBB80 of TM4SF superfamily.  
PN WO9831799-A2.  
PD 23-JUL-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.4%; Score 126; DB 2; Length 201;  
Best Local Similarity 21.8%; Pred. No. 9.6e-06;  
RESULT 694  
ID ABU03461 standard; protein; 201 AA.  
DE Angiogenesis-associated human protein sequence #6.  
PN WO200279492-A2.  
PD 10-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 10.4%; Score 126; DB 6; Length 201;  
Best Local Similarity 21.8%; Pred. No. 9.6e-06;  
RESULT 695  
ID ABW01508 standard; protein; 201 AA.  
DE Human receptor protein from clone HUVBB80.  
PN US2003129696-A1.  
PD 10-JUL-2003.  
PA (NIJ/) NI J.  
PA (ROSE/) ROSEN C A.  
PA (GENT/) GENTZ R.  
Query Match 10.4%; Score 126; DB 7; Length 201;  
Best Local Similarity 21.8%; Pred. No. 9.6e-06;  
RESULT 696

ID ADN38692 standard; protein; 201 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:10.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 10.4%; Score 126; DB 7; Length 201;  
Best Local Similarity 21.8%; Pred. No. 9.6e-06;  
RESULT 697  
ID AAM80948 standard; protein; 205 AA.  
DE Amino acid sequence of the human integral membrane protein-2.  
PN WO9846752-A1.  
PD 22-OCT-1998.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 10.3%; Score 125; DB 2; Length 205;  
Best Local Similarity 21.8%; Pred. No. 1.3e-05;  
RESULT 698  
ID AAB34200 standard; protein; 202 AA.  
DE Human secreted protein sequence encoded by gene 36 SEQ ID NO:168.  
PN WO200056755-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 122; DB 3; Length 202;  
Best Local Similarity 23.2%; Pred. No. 2.8e-05;  
RESULT 699  
ID AAU30786 standard; protein; 226 AA.  
DE Novel human secreted protein #1277.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.0%; Score 121; DB 4; Length 226;  
Best Local Similarity 25.5%; Pred. No. 4.3e-05;  
RESULT 700  
ID AAY12177 standard; protein; 122 AA.  
DE Human 5' EST secreted protein SEQ ID NO: 490.  
PN WO9906554-A2.  
PD 11-FEB-1999.  
PA (GEST-) GENSET.  
Query Match 9.9%; Score 120; DB 2; Length 122;  
Best Local Similarity 28.8%; Pred. No. 2.4e-05;  
RESULT 701  
ID AAY12854 standard; protein; 136 AA.  
DE Human 5' EST secreted protein SEQ ID NO:444.  
PN WO9906554-A2.  
PD 11-FEB-1999.  
PA (GEST-) GENSET.  
Query Match 9.9%; Score 120; DB 2; Length 136;  
Best Local Similarity 28.8%; Pred. No. 2.8e-05;  
RESULT 702  
ID AAY12178 standard; protein; 150 AA.  
DE Human 5' EST secreted protein SEQ ID NO: 491.  
PN WO9906554-A2.  
PD 11-FEB-1999.  
PA (GEST-) GENSET.  
Query Match 9.9%; Score 120; DB 2; Length 150;  
Best Local Similarity 28.8%; Pred. No. 3.2e-05;  
RESULT 703  
ID AAB64612 standard; protein; 108 AA.  
DE Human secreted protein BLAST search protein SEQ ID NO: 122.  
PN WO200077197-A1.  
PD 21-DEC-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 119.5; DB 4; Length 108;  
Best Local Similarity 33.7%; Pred. No. 2.3e-05;  
RESULT 704  
ID AAB64564 standard; protein; 180 AA.  
DE Human secreted protein #16.  
PN WO200077197-A1.  
PD 21-DEC-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 119.5; DB 4; Length 180;  
Best Local Similarity 33.7%; Pred. No. 4.7e-05;

RESULT 705  
ID ABP76262 standard; protein; 109 AA.  
DE Human GENSET protein SEQ ID 812.  
PN WO200283898-A1.  
PD 24-OCT-2002.  
PA (GEST-) GENSET.  
Query Match 9.4%; Score 114.5; DB 6; Length 109;  
Best Local Similarity 33.3%; Pred. No. 8.8e-05;  
RESULT 706  
ID AAB64611 standard; protein; 108 AA.  
DE Human secreted protein BLAST search protein SEQ ID NO: 121.  
PN WO200077197-A1.  
PD 21-DEC-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.3%; Score 113.5; DB 4; Length 108;  
Best Local Similarity 33.7%; Pred. No. 0.00011;  
RESULT 707  
ID AAM64540 standard; protein; 209 AA.  
DE Human fibrosarcoma cell line HT-1080 clone HP10034 protein.  
PN WO9821328-A2.  
PD 22-MAY-1998.  
PA (SAGA) SAGAMI CHEM RES CENTRE.  
Query Match 9.2%; Score 111.5; DB 2; Length 209;  
Best Local Similarity 20.2%; Pred. No. 0.00049;  
RESULT 708  
ID AAM51208 standard; protein; 209 AA.  
DE Human osteoclast expressed polypeptide SEQ ID NO 2.  
PN JP2001231573-A.  
PD 28-AUG-2001.  
PA (SHIO) SHIONOGI & CO LTD.  
Query Match 9.2%; Score 111.5; DB 4; Length 209;  
Best Local Similarity 20.2%; Pred. No. 0.00049;  
RESULT 709  
ID AAU29953 standard; protein; 107 AA.  
DE Novel human secreted protein #444.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 8.6%; Score 105; DB 4; Length 107;  
Best Local Similarity 31.2%; Pred. No. 0.0011;  
RESULT 710  
ID ADP66649 standard; protein; 450 AA.  
DE Mouse GHB receptor related polypeptide.  
PN WO2004046315-A2.  
PD 03-JUN-2004.  
PA (SLOW-) SLOWAVE INC.  
Query Match 8.3%; Score 101; DB 8; Length 450;  
Best Local Similarity 23.0%; Pred. No. 0.024;  
RESULT 711  
ID AAY11655 standard; protein; 86 AA.  
DE Human 5' EST secreted protein SEQ ID NO:307.  
PN WO9906439-A2.  
PD 11-FEB-1999.  
PA (GEST-) GENSET.  
Query Match 7.9%; Score 95.5; DB 2; Length 86;  
Best Local Similarity 32.9%; Pred. No. 0.01;  
RESULT 712  
ID ADP66647 standard; protein; 450 AA.  
DE Rat GHB receptor related polypeptide.  
PN WO2004046315-A2.  
PD 03-JUN-2004.  
PA (SLOW-) SLOWAVE INC.  
Query Match 7.7%; Score 93; DB 8; Length 450;  
Best Local Similarity 23.7%; Pred. No. 0.21;  
RESULT 713  
ID ABG29044 standard; protein; 426 AA.  
DE Novel human diagnostic protein #29035.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.4%; Score 90.5; DB 4; Length 426;

Best Local Similarity 30.8%; Pred. No. 0.37;  
RESULT 714  
ID ABG24776 standard; protein; 708 AA.  
DE Novel human diagnostic protein #24767.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 30.8%; Pred. No. 0.76; Length 708;  
RESULT 715  
ID ABG29047 standard; protein; 997 AA.  
DE Novel human diagnostic protein #29038.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 30.8%; Pred. No. 1.2; Length 997;  
RESULT 716  
ID ABG24324 standard; protein; 1118 AA.  
DE Novel human diagnostic protein #24315.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 30.8%; Pred. No. 1.5; Length 1118;  
RESULT 717  
ID ABU49046 standard; protein; 1036 AA.  
DE Protein encoded by Prokaryotic essential gene #34573.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 31.5%; Pred. No. 2.6; Length 1036;  
RESULT 718  
ID ADB65669 standard; protein; 117 AA.  
DE Human protein encoded by clone TRACH20011540.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match  
Best Local Similarity 23.0%; Pred. No. 0.13; Length 117;  
RESULT 719  
ID AAU30827 standard; protein; 185 AA.  
DE Novel human secreted protein #1318.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 28.1%; Pred. No. 0.25; Length 185;  
RESULT 720  
ID ADJ48738 standard; protein; 1174 AA.  
DE Oil-associated gene related protein #238.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDBAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match  
Best Local Similarity 20.8%; Pred. No. 4; Length 1174;  
RESULT 721  
ID ABU49666 standard; protein; 891 AA.  
DE Protein encoded by Prokaryotic essential gene #35193.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 22.6%; Pred. No. 3.1; Length 891;  
RESULT 722  
ID ABB48024 standard; protein; 283 AA.  
DE Listeria monocytogenes protein #728.

PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP ) INST PASTEUR.  
Query Match  
Best Local Similarity 24.7%; Pred. No. 0.69; Length 283;  
RESULT 723  
ID AAW98770 standard; protein; 449 AA.  
DE H. pylori GHPO 1130 protein.  
PN WO9843478-A1.  
PD 08-OCT-1998.  
PA (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 31.5%; Pred. No. 1.3; Length 449;  
RESULT 724  
ID AAY59127 standard; protein; 271 AA.  
DE Protein encoded by V. cholerae thxA gene 5' flanking region.  
PN WO9961634-A1.  
PD 02-DEC-1999.  
PA (SBLV-) SBL VACCIN AB.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 0.75; Length 271;  
RESULT 725  
ID AAW52812 standard; protein; 344 AA.  
DE Human induced tumour protein.  
PN WO9806846-A1.  
PD 19-FEB-1998.  
PA (INCY-) INCYTE PHARM INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1; Length 344;  
RESULT 726  
ID AAY07771 standard; protein; 356 AA.  
DE Human secreted protein fragment encoded from gene 28.  
PN WO9909155-A1.  
PD 25-FEB-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 2; Length 356;  
RESULT 727  
ID AAY95015 standard; protein; 453 AA.  
DE Human secreted protein vc61\_1, SEQ ID NO:70.  
PN WO200011015-A1.  
PD 02-MAR-2000.  
PA (ALPH-) ALPHAGENE INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 728  
ID AAG65236 standard; protein; 453 AA.  
DE Protein tyrosine kinase 50.  
PN CN1298944-A.  
PD 13-JUN-2001.  
PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 4; Length 453;  
RESULT 729  
ID AAU29065 standard; protein; 453 AA.  
DE Human PRO polypeptide sequence #42.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 730  
ID AAM39489 standard; protein; 453 AA.  
DE Human polypeptide SEQ ID NO 2634.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 4; Length 453;  
RESULT 731  
ID AAB65170 standard; protein; 453 AA.  
DE Human PRO732 (UNQ396) protein sequence SEQ ID NO:73.

PN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 4; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 732  
ID ABB90299 standard; protein; 453 AA.  
DE Human polypeptide SEQ ID NO 2675.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 5; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 733  
ID ABUS8441 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 734  
ID ABUS7989 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 735  
ID ABUS4304 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 736  
ID ABR66178 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 737  
ID ABR65568 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 738  
ID ABUS9508 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 739  
ID ABUS7985 standard; protein; 453 AA.  
DE Human PRO polypeptide #17.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 740  
ID ABUS9063 standard; protein; 453 AA.  
DE Novel human secreted or transmembrane protein PRO732.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 741  
ID ABUS2575 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PD 06-FEB-2003.

PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 742  
ID ABUS2747 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 743  
ID ABUS9868 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003036147-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 744  
ID ABR68117 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 745  
ID ABUS60494 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein, #24.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 746  
ID ABUS6170 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 747  
ID ABUS92601 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 748  
ID ABO08678 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 749  
ID ABO02730 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 750  
ID ABR74884 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 7.0%; Score 85.5; DB 6; Length 453;  
PD 23.1%; Pred. No. 1.5;  
RESULT 751  
ID ABR94646 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003044926-A1.  
PD 06-MAR-2003.



Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 752  
ID ABU13876 standard; protein; 453 AA.  
DE Human PRO732 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 753  
ID ABU85619 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 754  
ID ABU98779 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 755  
ID ABU97994 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 756  
ID ABU91700 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 757  
ID ABU89393 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 758  
ID ABU86234 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 759  
ID ABU67447 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 760  
ID ABU80475 standard; protein; 453 AA.  
DE Human PRO protein #42.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 761  
ID ABU72461 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.

PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 762  
ID ABR99393 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 763  
ID ABR98783 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 764  
ID ABO16306 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 765  
ID ABR92206 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 766  
ID ABO18847 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 767  
ID ABR78268 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 768  
ID ABU85004 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 769  
ID ABO00143 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 770  
ID ABO11475 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 771  
ID ABO02120 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003040054-A1.

PD 27-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 772  
ID ABU88694 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 773  
ID ABU83389 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 774  
ID ABO06190 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 775  
ID ABR59226 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 776  
ID ABO09288 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 777  
ID ABO19152 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 778  
ID ABO11170 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 779  
ID ABR66788 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 780  
ID ABO16001 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 781  
ID ABO13707 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;

Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 782  
ID ABU65610 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein, SEQ ID 84.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 783  
ID ABO07458 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 784  
ID ABO03645 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 785  
ID ABR67093 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 786  
ID ABO15696 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 787  
ID ABU55977 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein, PRO732.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 788  
ID ABU65305 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 789  
ID ABU95250 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 790  
ID ABU71153 standard; protein; 453 AA.  
DE Human PRO732 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 791  
ID ABO07763 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
RESULT 792

ID ABR70004 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 793  
ID ABR69337 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 794  
ID ABO01478 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 795  
ID ABU81280 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 796  
ID ABR60077 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 797  
ID ABR67812 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 798  
ID ABR65200 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 799  
ID ABR68422 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 800  
ID ABR71834 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 801  
ID ABU59210 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein, #24.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 802

ID ABU85314 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 803  
ID ABU89004 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 804  
ID ABU83084 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 805  
ID ABU94940 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 806  
ID ABU90488 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 807  
ID ABU83999 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 808  
ID ABU93650 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 809  
ID ABO25907 standard; protein; 453 AA.  
DE Human PRO732 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 810  
ID ABR64895 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 811  
ID ABR68727 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 812  
ID ABO06543 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.  
 PN US2003036125-A1.  
 PD 20-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 813  
 ID ABR99088 standard; protein; 453 AA.  
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
 PN US2003040068-A1.  
 PD 27-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 814  
 ID ABU56972 standard; protein; 453 AA.  
 DE Human PRO polypeptide #42.  
 PN US2003027280-A1.  
 PD 06-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 815  
 ID ABU85924 standard; protein; 453 AA.  
 DE Novel human secreted and transmembrane protein PRO732.  
 PN US2003022300-A1.  
 PD 30-JAN-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 816  
 ID ABU82211 standard; protein; 453 AA.  
 DE Novel human secreted and transmembrane protein PRO732.  
 PN US2003036136-A1.  
 PD 20-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 817  
 ID ABU87222 standard; protein; 453 AA.  
 DE Human PRO polypeptide #42.  
 PN US2003036138-A1.  
 PD 20-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 818  
 ID ABU83694 standard; protein; 453 AA.  
 DE Human secreted/transmembrane protein (PRO) #42.  
 PN US2003032109-A1.  
 PD 13-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 819  
 ID ABO08068 standard; protein; 453 AA.  
 DE Human PRO polypeptide #42.  
 PN US2003040066-A1.  
 PD 27-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 820  
 ID ABU81779 standard; protein; 453 AA.  
 DE Novel human secreted and transmembrane protein PRO732.  
 PN US2003032104-A1.  
 PD 13-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 821  
 ID ABU65943 standard; protein; 453 AA.  
 DE Novel human secreted and transmembrane protein PRO732.  
 PN US2003036157-A1.  
 PD 20-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 822  
 ID ABR59772 standard; protein; 453 AA.  
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
 PN US2003032120-A1.  
 PD 13-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 823  
 ID ABU93960 standard; protein; 453 AA.  
 DE Novel human secreted and transmembrane protein PRO732.  
 PN US2003036155-A1.  
 PD 20-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 824  
 ID ABU99813 standard; protein; 453 AA.  
 DE Novel human secreted and transmembrane protein PRO732.  
 PN US2003022296-A1.  
 PD 30-JAN-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 825  
 ID ABR66483 standard; protein; 453 AA.  
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
 PN US2003027281-A1.  
 PD 06-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

PA (GETH ) GENENTECH INC.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 826  
 ID ABR90901 standard; protein; 453 AA.  
 DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
 PN US2003040058-A1.  
 PD 27-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 827  
 ID ABU58916 standard; protein; 453 AA.  
 DE Human secreted/transmembrane protein, #24.  
 PN US2002142961-A1.  
 PD 03-OCT-2002.

PA (GETH ) GENENTECH INC.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 828  
 ID ABU94328 standard; protein; 453 AA.  
 DE Human PRO polypeptide #42.  
 PN US2003017540-A1.  
 PD 23-JAN-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 829  
 ID ABU79210 standard; protein; 453 AA.  
 DE Human PRO polypeptide #42.  
 PN US2003032106-A1.  
 PD 13-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 830  
 ID ABU86539 standard; protein; 453 AA.  
 DE Human secreted/transmembrane protein (PRO) #42.  
 PN US2003032129-A1.  
 PD 13-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 831  
 ID ABU86844 standard; protein; 453 AA.  
 DE Novel human secreted and transmembrane protein PRO732.  
 PN US2003032131-A1.  
 PD 13-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

RESULT 832  
 ID ABU94633 standard; protein; 453 AA.  
 DE Human PRO polypeptide #42.  
 PN US2003032103-A1.  
 PD 13-FEB-2003.

Query Match  
 Best Local Similarity 23.1%; Score 85.5; DB 6; Length 453;  
 Pred. No. 1.5;

Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 833  
ID ABO04560 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 834  
ID ABR70309 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 835  
ID ABU92294 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 836  
ID ABU98474 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 837  
ID ABR65873 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 838  
ID ABR64590 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 839  
ID ABU59359 standard; protein; 453 AA.  
DE Novel human secreted or transmembrane protein PRO1120.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 840  
ID ABU79515 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 841  
ID ABU92906 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 842  
ID ABU95865 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 843

ID ABU91085 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 844  
ID ABU90178 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 845  
ID ABO09593 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 846  
ID ABO10865 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 847  
ID ABR70919 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 848  
ID ABU87527 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 849  
ID ABU91395 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 850  
ID ABU84609 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 851  
ID ABR69699 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 852  
ID ABU80076 standard; protein; 453 AA.  
DE Human PRO protein #42.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 853  
ID ABU92125 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003017476-A1.



PD 23-JAN-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 854  
ID ABU93345 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 855  
ID ABO09898 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 856  
ID ABO08983 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 857  
ID ABU10831 standard; protein; 453 AA.  
DE Human PRO polypeptide #17.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 858  
ID ABU10551 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein #42.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 859  
ID ABU81583 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 860  
ID ABU95560 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 861  
ID ABU96769 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 862  
ID ABR70614 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 863  
ID ABO04965 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.

PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 864  
ID ABO08373 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 865  
ID ABU88522 standard; protein; 453 AA.  
DE Human secreted and transmembrane polypeptide PRO732.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 866  
ID ABO34036 standard; protein; 453 AA.  
DE Human PRO732 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 867  
ID ABO05580 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 868  
ID ABR73969 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 869  
ID ABR95561 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 870  
ID ABR80858 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 871  
ID ABR81163 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 872  
ID ABM00859 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;

RESULT 873  
ID ABR88461 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 874  
ID ABM77282 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 875  
ID ABO28766 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 876  
ID ABO31511 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 877  
ID ABM07928 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 878  
ID ABO40408 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 879  
ID ABO35833 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 880  
ID ABO43972 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 881  
ID ADA77836 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 882

ID ABM24767 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 883  
ID ABO03035 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 884  
ID ABR90291 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 885  
ID ABM17205 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 886  
ID ABR94951 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 887  
ID ABR95256 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 888  
ID ABO21494 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 889  
ID ABR97758 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 890  
ID ABR87546 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 891  
ID ABM77587 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 892  
ID ABM27817 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064440-A1.  
PD 03-APR-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 893  
ID ABM06098 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 894  
ID ABM03604 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 895  
ID ABM35055 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 896  
ID ABM26292 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 897  
ID ABO48074 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 898  
ID ABR92816 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 899  
ID ABO24577 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 900  
ID ADA37584 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;

RESULT 901  
ID ABM11588 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 902  
ID ABM02689 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 903  
ID ABM15985 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 904  
ID ABO27546 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 905  
ID ABM29037 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 906  
ID ABM07013 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 907  
ID ABM21107 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 908  
ID ABM09453 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 909  
ID ABO41323 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 910

ID ABO36138 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 911  
ID ABO43667 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 912  
ID ABM76367 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 913  
ID ABM76063 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 914  
ID ABM25682 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 915  
ID ABM25987 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 916  
ID ADA21270 standard; protein; 453 AA.  
DE Human secreted/transmembrane polypeptide PRO732.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 917  
ID ABO03340 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 918  
ID ABO02425 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 919  
ID ABR90596 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 920

ID ABR73664 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 921  
ID ABO16916 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 922  
ID ABR94341 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 923  
ID ABR75848 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 924  
ID ABR71224 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 925  
ID ABR93121 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 926  
ID ABR93426 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 927  
ID ADA10057 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein, PRO732.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 928  
ID ABR87851 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 929  
ID ABO27851 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003064454-A1.  
PD 03-APR-2003.

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PA (GETH ) GENENTECH INC. 7.0%; Score 85.5; DB 6; Length 453;
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 930
ID ABO29986 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 931
ID ABO33195 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 932
ID ABO04883 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 933
ID ABO08843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 934
ID ABO36443 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 935
ID ABO35528 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 936
ID ABO39493 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 937
ID ABM10368 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 938
ID ABM1893 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC. 7.0%; Score 85.5; DB 6; Length 453;
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 939
ID ABO52039 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 940
ID ABO52344 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 941
ID ABO23662 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 942
ID ADA17601 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 943
ID ABR97148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 944
ID ABR86936 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 945
ID ABM10978 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 946
ID ABM28122 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 947
ID ABO32121 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;
RESULT 948
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ID ABM15248 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 949  
ID ABM06403 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 950  
ID ABM04214 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 951  
ID ABM22327 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 952  
ID ABM07623 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 953  
ID ABO40713 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 954  
ID ABM35360 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 955  
ID ABM33123 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 956  
ID ABO52649 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 957  
ID ABO50209 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.

PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 958  
ID ABV99203 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 959  
ID ABO04255 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 960  
ID ABO05885 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 961  
ID ABM18425 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 962  
ID ADA27709 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 963  
ID ABR97453 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 964  
ID ABR80553 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 965  
ID ABM01164 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 966  
ID ABR88766 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073169-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 967

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ID ABM13418 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 968
ID ABM20802 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 969
ID ABQ41933 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 970
ID ABO42543 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 971
ID ABM10063 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 972
ID ABO38578 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 973
ID ABM32818 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 974
ID ABM22632 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 975
ID ABM74843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 976
ID ADA79628 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 977
ID ABR96233 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 978
ID ABM02384 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 979
ID ABR86326 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 980
ID ABR86631 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 981
ID ABM16595 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 982
ID ABM29647 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 983
ID ABO29071 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 984
ID ABM23852 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 985
ID ABM23242 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
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Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 986
ID ABM22022 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 987
ID ABO37663 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 988
ID ABM28427 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 989
ID ABM28732 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 990
ID ABM66376 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 991
ID ABM75758 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 992
ID ABM34038 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 993
ID ABM34343 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 994
ID ABO20274 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 995
ID ABO21189 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 996
ID ABO22104 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 997
ID ABR96538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 998
ID ADA94289 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 999
ID ABR85716 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1000
ID ABR99698 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1001
ID ABM00554 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1002
ID ABM00249 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1003
ID ABO29681 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1004
ID ABM23547 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
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RESULT 1005
ID ABO29342 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US200306879-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1006
ID ABO38273 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1007
ID ABO45573 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1008
ID ABO20497 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1009
ID ADA81355 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1010
ID ABO16611 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1011
ID ABO18237 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1012
ID ABO22664 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1013
ID ABO22969 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1014
ID ABR92511 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1015
ID ABR81468 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1016
ID ABR77892 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1017
ID ABR89681 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1018
ID ABR26597 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1019
ID ABR13723 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1020
ID ABO28461 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1021
ID ABO30291 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1022
ID ABR07318 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1023
ID ABR03909 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
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Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1024  
ID ABO37053 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1025  
ID ABO41628 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1026  
ID ABO35223 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1027  
ID ABM25072 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1028  
ID ABO47464 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1029  
ID ABO47769 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1030  
ID ABO48379 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1031  
ID ABO51429 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1032  
ID ABO51734 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1033

ID ABO50514 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1034  
ID ABR79638 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1035  
ID ABM16900 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1036  
ID ABO17932 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1037  
ID ABO20884 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1038  
ID ABR96843 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1039  
ID ADA38514 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1040  
ID ABM12198 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1041  
ID ABM16290 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1042  
ID ABM24157 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064441-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1043



Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1043  
ID ABM14638 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1044  
ID ABM04519 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1045  
ID ABM06708 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1046  
ID ABM09148 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1047  
ID ABO39188 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1048  
ID ABM75453 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1049  
ID ABM25377 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1050  
ID ABM19887 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1051  
ID ABO46793 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1052  
ID ABO47098 standard; protein; 453 AA.

DE Human PRO polypeptide #42.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1053  
ID ADA83153 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1054  
ID ABR71529 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1055  
ID ABR72139 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1056  
ID ABR98478 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1057  
ID ABO06848 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1058  
ID ABR84801 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1059  
ID ABR73359 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1060  
ID ABR76453 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1061  
ID ABR73054 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1062  
ID ABM18120 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1063  
ID ABO20579 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1064  
ID ABO25322 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1065  
ID ABO25627 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1066  
ID ABR94036 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1067  
ID ADA92635 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1068  
ID ABR79943 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1069  
ID ABM11283 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1070  
ID ABO32890 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1071  
ID ABO30596 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1072  
ID ABO30901 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1073  
ID ABM27207 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1074  
ID ABM29952 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1075  
ID ABM05488 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1076  
ID ABM15553 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1077  
ID ABM08538 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1078  
ID ABO42238 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1079  
ID ABO37968 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1080  
ID ABO45878 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 6; Length 453;

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Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1081
ID ABM66681 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US200306868-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1082
ID ADB20196 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1083
ID ABM19582 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1084
ID ABO49294 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1085
ID ABO49599 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1086
ID ADA78448 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1087
ID ABR88156 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1088
ID ABM26902 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1089
ID ABM03299 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1090
ID ABO39798 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 6; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1091
ID ABO49904 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1092
ID ABO50819 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1093
ID ABO05275 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1094
ID ABR74579 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1095
ID ABR77058 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1096
ID ABM17815 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1097
ID ABR95866 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1098
ID ABO21799 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1099
ID ABO19969 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
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RESULT 1100  
ID ABO24272 standard; protein; 453 AA.  
DE Human secreted/cranmembrane protein (PRO) #42.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1101  
ID ABR86021 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1102  
ID ABM10673 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1103  
ID ABM76672 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1104  
ID ABR89376 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073170-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1105  
ID ABM12503 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1106  
ID ABM05793 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1107  
ID ABO34918 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003068728-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1108  
ID ABM02994 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1109  
ID ABM18972 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1110  
ID ABM19277 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1111  
ID ABO46488 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1112  
ID ABO48989 standard; protein; 453 AA.  
DE Human secreted/cranmembrane protein (PRO) #42.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1113  
ID ABR69032 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1114  
ID ABR89071 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1115  
ID ABR72444 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1116  
ID ABR74274 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1117  
ID ABO18542 standard; protein; 453 AA.  
DE Human secreted/cranmembrane protein (PRO) #42.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1118  
ID ABR80248 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;

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Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1119
ID ABM01469 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1120
ID ABM02079 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1121
ID ABR87241 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1122
ID ABM12808 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1123
ID ABM30562 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1124
ID ABM24462 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1125
ID ABO29376 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1126
ID ABO31206 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1127
ID ABM14333 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1128
ID ABM09758 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1129
ID ABO38883 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1130
ID ABM34648 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1131
ID ABO51124 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1132
ID ABO03950 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1133
ID ABO10420 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1134
ID ABO53122 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1135
ID ABR77663 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1136
ID ABR78873 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054456-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1137
ID ABO23967 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.0%; Score 85.5; DB 7; Length 453;
Best Local Similarity 23.1%; Pred. No. 1.5;
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Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1138  
ID ABR93731 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1139  
ID ABM01774 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1140  
ID ABM78197 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1141  
ID ABR89986 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1142  
ID ADA22196 standard; protein; 453 AA.  
DE Human secreted/transmembrane polypeptide PRO732.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1143  
ID ABM27512 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1144  
ID ABM13113 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1145  
ID ABO31816 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1146  
ID ABM14028 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1147  
ID ABM08233 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1148  
ID ABO40103 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1149  
ID ABM74538 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1150  
ID ABM33733 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1151  
ID ABM20192 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1152  
ID ABO48684 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1153  
ID ABO22492 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1154  
ID ABR72749 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1155  
ID ABO15391 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1156  
ID ABR85106 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;

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Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1157
ID ABO15086 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1158
ID ABO17221 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1159
ID ABM17510 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1160
ID ADA06362 standard; protein; 453 AA.
DE Human secreted/transmembrane PRO polypeptide #17.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1161
ID ADA39055 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1162
ID ABR85411 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1163
ID ABM76977 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1164
ID ABO28156 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1165
ID ABM22937 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1166
ID ABM30257 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1167
ID ABM21717 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1168
ID ABM21412 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1169
ID ABM14943 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1170
ID ABO41018 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1171
ID ABO36748 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1172
ID ABO37358 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1173
ID ABM75148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1174
ID ABM33428 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.1%; Pred. No. 1.5;
RESULT 1175
ID ABO46183 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
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Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1176  
ID ADA82519 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1177  
ID ADB96081 standard; protein; 453 AA.  
DE Human PRO polypeptide #17.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1178  
ID ABM31782 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068680-A1.  
PD 10-APR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1179  
ID ABM31172 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1180  
ID ADB85827 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1181  
ID ABM32087 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1182  
ID ABM32392 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1183  
ID ABM31477 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1184  
ID ABM30867 standard; protein; 453 AA.  
DE Human secreted polypeptide PRO732, SEQ ID NO:84.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1185

ID ADC57553 standard; protein; 453 AA.  
DE Human PRO polypeptide #17.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1186  
ID ADC54917 standard; protein; 453 AA.  
DE Human PRO polypeptide #17.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1187  
ID ADC11784 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1188  
ID ADC56206 standard; protein; 453 AA.  
DE Human PRO polypeptide #17.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1189  
ID ADC07261 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1190  
ID ADC11251 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1191  
ID ADC14373 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1192  
ID ADD07905 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1193  
ID ADC81730 standard; protein; 453 AA.  
DE Human PRO polypeptide #17.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1194  
ID ADD07372 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1195  
ID ADC77580 standard; protein; 453 AA.  
DE Human TMS2 amino acid sequence.

PN WO2003066829-A2.  
PD 14-AUG-2003.  
PA (DISC-) DISCOVERY GENOMICS INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1196  
ID ADC82263 standard; protein; 453 AA.  
DE Human PRO polypeptide #17.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1197  
ID ADD05557 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1198  
ID ADD08443 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1199  
ID ADD06692 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1200  
ID ADC82939 standard; protein; 453 AA.  
DE Human PRO polypeptide #17.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1201  
ID ADD55046 standard; protein; 453 AA.  
DE Human PRO polypeptide #17.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1202  
ID ADD56004 standard; protein; 453 AA.  
DE Human PRO polypeptide #17.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1203  
ID ADD54442 standard; protein; 453 AA.  
DE Human PRO polypeptide #17.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1204  
ID ADE26596 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1205  
ID ADE26063 standard; protein; 453 AA.

DE Novel human secreted and transmembrane protein PRO732.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1206  
ID ADF67000 standard; protein; 453 AA.  
DE Human PRO732 amino acid sequence SEQ ID NO:73.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1207  
ID ADG02552 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1208  
ID ADG01259 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1209  
ID ADF95434 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1210  
ID ADG12249 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1211  
ID ADH08909 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1212  
ID ADI35254 standard; protein; 453 AA.  
DE Human PRO polypeptide #17.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1213  
ID ADH99746 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1214  
ID ADL32690 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 7; Length 453;

Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1215  
ID ADM30224 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1216  
ID ADE74221 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1217  
ID ADE74833 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein (PRO) #42.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1218  
ID ADF35199 standard; protein; 453 AA.  
DE Human PRO732 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1219  
ID ADG11449 standard; protein; 453 AA.  
DE Human PRO732 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1220  
ID ADF96046 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1221  
ID ADG04317 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1222  
ID ADG00477 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1223  
ID ADG82733 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1224  
ID ADH26014 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2003068770-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1225  
ID ADH19319 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1226  
ID ADH32983 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1227  
ID ADH20812 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1228  
ID ADH19852 standard; protein; 453 AA.  
DE Human secreted/transmembrane protein PRO732.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1229  
ID ADJ54722 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1230  
ID ADJ64493 standard; protein; 453 AA.  
DE Human PRO polypeptide #42.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1231  
ID ADM31389 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1232  
ID ADM36436 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1.5; Length 453;  
RESULT 1233  
ID ADM40241 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.



Query Match 7.0%; Score 85.5; DB 8; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1234  
ID ADN37849 standard; protein; 453 AA.  
DE Novel human secreted and transmembrane protein PRO732.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 8; Length 453;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
RESULT 1235  
ID AAY66647 standard; protein; 455 AA.  
DE Membrane-bound protein PRO732.  
PN WO9963088-A2.  
PD 09-DEC-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 85.5; DB 3; Length 455;  
Best Local Similarity 23.1%; Pred. No. 1.6;  
RESULT 1236  
ID ADG10618 standard; protein; 472 AA.  
DE Human STAT6-activating protein, SEQ ID NO:208.  
PN WO200296943-A1.  
PD 05-DEC-2002.  
PA (ASAH ) ASAH KASEI KOGYO KK.  
Query Match 7.0%; Score 85.5; DB 7; Length 472;  
Best Local Similarity 23.1%; Pred. No. 1.6;  
RESULT 1237  
ID AAM41275 standard; protein; 477 AA.  
DE Human polypeptide SEQ ID NO 6206.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.0%; Score 85.5; DB 4; Length 477;  
Best Local Similarity 23.1%; Pred. No. 1.7;  
RESULT 1238  
ID AAG72466 standard; protein; 318 AA.  
DE Human OR-like polypeptide query sequence, SEQ ID NO: 2147.  
PN WO200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
Query Match 7.0%; Score 85; DB 4; Length 318;  
Best Local Similarity 19.5%; Pred. No. 1.1;  
RESULT 1239  
ID AAG71752 standard; protein; 318 AA.  
DE Human olfactory receptor polypeptide, SEQ ID NO: 1433.  
PN WO200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
Query Match 7.0%; Score 85; DB 4; Length 318;  
Best Local Similarity 19.5%; Pred. No. 1.1;  
RESULT 1240  
ID AAU31533 standard; protein; 450 AA.  
DE Novel human secreted protein #2024.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.0%; Score 85; DB 4; Length 450;  
Best Local Similarity 25.6%; Pred. No. 1.7;  
RESULT 1241  
ID AAY11065 standard; protein; 449 AA.  
DE H. pylori ORF 09cp10713\_36359687\_c1\_119 inner membrane protein.  
PN WO9824475-A1.  
PD 11-JUN-1998.  
PA (ASTR ) ASTRA AB.  
Query Match 6.9%; Score 84; DB 2; Length 449;  
Best Local Similarity 31.5%; Pred. No. 2.3;  
RESULT 1242  
ID ADO78101 standard; protein; 261 AA.  
DE Human Claudin-18A2.1.  
PN DE10254601-A1.  
PD 03-JUN-2004.

PA (GANY-) GANYMED PHARM AG.  
Query Match 6.9%; Score 83.5; DB 8; Length 261;  
Best Local Similarity 25.6%; Pred. No. 1.2;  
RESULT 1243  
ID ADL95659 standard; protein; 316 AA.  
DE Human novel GPCR1c.  
PN US2003165829-A1.  
PD 04-SEP-2003.  
PA (PADI/) PADIGARU M.  
PA (MAJU/) MAJUMDER K.  
PA (BURG/) BURGESS C E.  
PA (VERN/) VERNET C A M.  
PA (FERN/) FERNANDES E R.  
PA (SHIM/) SHIMKETS R A.  
PA (TCHN/) TCHERNEV V T.  
PA (MISH/) MISHRA V.  
PA (CASM/) CASMAN S.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
Query Match 6.9%; Score 83.5; DB 7; Length 316;  
Best Local Similarity 22.1%; Pred. No. 1.6;  
RESULT 1244  
ID AAB90779 standard; protein; 180 AA.  
DE Human shear stress-response protein SEQ ID NO: 58.  
PN WO200125427-A1.  
PD 12-APR-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
PA (NOJI/) NOJIMA H.  
Query Match 6.8%; Score 82.5; DB 4; Length 180;  
Best Local Similarity 27.4%; Pred. No. 0.93;  
RESULT 1245  
ID ADE83497 standard; protein; 180 AA.  
DE Human Protein P53801, SEQ ID NO 11093.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 6.8%; Score 82.5; DB 7; Length 180;  
Best Local Similarity 27.4%; Pred. No. 0.93;  
RESULT 1246  
ID AAB58380 standard; protein; 185 AA.  
DE Lung cancer associated polypeptide sequence SEQ ID 718.  
PN WO200055180-A2.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
Query Match 6.8%; Score 82.5; DB 3; Length 185;  
Best Local Similarity 27.4%; Pred. No. 0.97;  
RESULT 1247  
ID AAE07073 standard; protein; 261 AA.  
DE Human gene 1 encoded secreted protein HTPFX16, SEQ ID NO:90.  
PN WO200154708-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.8%; Score 82.5; DB 4; Length 261;  
Best Local Similarity 25.8%; Pred. No. 1.6;  
RESULT 1248  
ID ABG65079 standard; protein; 261 AA.  
DE Human albumin fusion protein #1754.  
PN WO200177137-A1.  
PD 18-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.8%; Score 82.5; DB 5; Length 261;  
Best Local Similarity 25.8%; Pred. No. 1.6;  
RESULT 1249  
ID ADL78346 standard; protein; 261 AA.  
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1828.  
PN US2004010134-A1.  
PD 15-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (HASE/) HASELTINE W A.  
Query Match 6.8%; Score 82.5; DB 8; Length 261;  
Best Local Similarity 25.8%; Pred. No. 1.6;

RESULT 1250  
ID ADG42639 standard; protein; 867 AA.  
DE Mouse prominin 1 precursor.  
PN US2003204052-A1.  
PD 30-OCT-2003.  
PA (HERR/) HERRMANN J L.  
PA (RAST/) RASTELLI L.  
PA (SHIM/) SHIMKETS R A.  
Query Match 6.7%; Score 82; DB 7; Length 867;  
Best Local Similarity 25.0%; Pred. No. 9.9;  
RESULT 1251  
ID AAE07051 standard; protein; 261 AA.  
DE Human gene 1 encoded secreted protein HTPFX16, SEQ ID NO:68.  
PN WO200154708-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.7%; Score 81.5; DB 4; Length 261;  
Best Local Similarity 25.6%; Pred. No. 2.1;  
RESULT 1252  
ID ABG65078 standard; protein; 261 AA.  
DE Human albumin fusion protein #1753.  
PN WO200177137-A1.  
PD 18-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.7%; Score 81.5; DB 5; Length 261;  
Best Local Similarity 25.6%; Pred. No. 2.1;  
RESULT 1253  
ID ADL78345 standard; protein; 261 AA.  
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1827.  
PN US2004010134-A1.  
PD 15-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (HASE/) HASELTINE W A.  
Query Match 6.7%; Score 81.5; DB 8; Length 261;  
Best Local Similarity 25.6%; Pred. No. 2.1;  
RESULT 1254  
ID AAE07106 standard; protein; 276 AA.  
DE Human gene 1 encoded secreted protein fragment, SEQ ID NO:123.  
PN WO200154708-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.7%; Score 81.5; DB 4; Length 276;  
Best Local Similarity 25.6%; Pred. No. 2.2;  
RESULT 1255  
ID AAE10682 standard; protein; 316 AA.  
DE G-protein coupled receptor 1c (GPCR1c).  
PN WO200164879-A2.  
PD 07-SEP-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.7%; Score 81.5; DB 4; Length 316;  
Best Local Similarity 21.8%; Pred. No. 2.7;  
RESULT 1256  
ID AAE09449 standard; protein; 1694 AA.  
DE Human sbg24878Sia protein #2.  
PN WO200160850-A1.  
PD 23-AUG-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
Query Match 6.7%; Score 81.5; DB 4; Length 1694;  
Best Local Similarity 22.7%; Pred. No. 29;  
RESULT 1257  
ID AAE09448 standard; protein; 1709 AA.  
DE Human sbg24878Sia protein #1.  
PN WO200160850-A1.  
PD 23-AUG-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
Query Match 6.7%; Score 81.5; DB 4; Length 1709;  
Best Local Similarity 22.7%; Pred. No. 30;  
RESULT 1258  
ID ABG10466 standard; protein; 1839 AA.  
DE Novel human diagnostic protein #10457.  
PN WO200175067-A2.

PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.7%; Score 81.5; DB 4; Length 1839;  
Best Local Similarity 22.7%; Pred. No. 33;  
RESULT 1259  
ID AAR13274 standard; protein; 254 AA.  
DE Petunia extracellular chitinase.  
PN EP440304-A.  
PD 07-AUG-1991.  
PA (MOGE-) MOGEN INT NV.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 6.7%; Score 81; DB 2; Length 254;  
Best Local Similarity 24.0%; Pred. No. 2.3;  
RESULT 1260  
ID AAW31296 standard; protein; 254 AA.  
DE Petunia hybrida extracellular chitinase protein.  
PN US5670706-A.  
PD 23-SEP-1997.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
PA (MOGE-) MOGEN INT NV.  
Query Match 6.7%; Score 81; DB 2; Length 254;  
Best Local Similarity 24.0%; Pred. No. 2.3;  
RESULT 1261  
ID AAB07512 standard; protein; 254 AA.  
DE Amino acid sequence of an extracellular chitinase.  
PN US6087560-A.  
PD 11-JUL-2000.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
PA (MOGE-) MOGEN INT NV.  
Query Match 6.7%; Score 81; DB 3; Length 254;  
Best Local Similarity 24.0%; Pred. No. 2.3;  
RESULT 1262  
ID AAY12855 standard; protein; 82 AA.  
DE Human 5' EST secreted protein SEQ ID NO:445.  
PN WO9906549-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 6.6%; Score 80.5; DB 2; Length 82;  
Best Local Similarity 28.8%; Pred. No. 0.52;  
RESULT 1263  
ID AAG71984 standard; protein; 320 AA.  
DE Human olfactory receptor polypeptide, SEQ ID NO: 1665.  
PN WO200127158-A2.  
PD 19-APR-2001.  
PA (DIGI-) DIGISCENTS.  
PA (YEDA ) YEDA RES & DEV CO LTD.  
Query Match 6.6%; Score 80.5; DB 4; Length 320;  
Best Local Similarity 22.5%; Pred. No. 3.6;  
RESULT 1264  
ID ABM69560 standard; protein; 157 AA.  
DE Photorhabdus luminescens protein sequence #2657.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.6%; Score 80; DB 6; Length 157;  
Best Local Similarity 29.2%; Pred. No. 1.5;  
RESULT 1265  
ID ABW70252 standard; protein; 391 AA.  
DE Photorhabdus luminescens protein sequence #3349.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.5%; Score 79.5; DB 6; Length 391;  
Best Local Similarity 21.6%; Pred. No. 6.2;  
RESULT 1266  
ID ABP38136 standard; protein; 430 AA.  
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:2981.  
PN US6380370-B1.  
PD 30-APR-2002.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.5%; Score 79.5; DB 5; Length 430;

Best Local Similarity 19.1%; Pred. No. 7.1;  
RESULT 1267  
ID ABB92528 standard; protein; 558 AA.  
DE Herbicidally active polypeptide SEQ ID NO 1739.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB ) BAYER AG.  
Query Match 6.5%; Score 79.5; DB 5; Length 558;  
Best Local Similarity 22.7%; Pred. No. 10;  
RESULT 1268  
ID ABB93024 standard; protein; 1143 AA.  
DE Herbicidally active polypeptide SEQ ID NO 2235.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB ) BAYER AG.  
Query Match 6.5%; Score 79.5; DB 5; Length 1143;  
Best Local Similarity 24.6%; Pred. No. 29;  
RESULT 1269  
ID ADA35539 standard; protein; 1160 AA.  
DE Acinetobacter baumannii protein #2700.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.5%; Score 79.5; DB 6; Length 1160;  
Best Local Similarity 22.8%; Pred. No. 29;  
RESULT 1270  
ID ADM04158 standard; protein; 144 AA.  
DE Human protein of the invention SEQ ID NO:2843.  
PN EP1347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 6.5%; Score 79; DB 7; Length 144;  
Best Local Similarity 27.8%; Pred. No. 1.7;  
RESULT 1271  
ID ABP40601 standard; protein; 315 AA.  
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5446.  
PN US6380370-B1.  
PD 30-APR-2002.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.5%; Score 79; DB 5; Length 315;  
Best Local Similarity 20.9%; Pred. No. 5.3;  
RESULT 1272  
ID ABU40824 standard; protein; 502 AA.  
DE Protein encoded by prokaryotic essential gene #26351.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.5%; Score 79; DB 6; Length 502;  
Best Local Similarity 21.4%; Pred. No. 10;  
RESULT 1273  
ID ABB68615 standard; protein; 546 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 32637.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 6.5%; Score 79; DB 4; Length 546;  
Best Local Similarity 20.9%; Pred. No. 11;  
RESULT 1274  
ID ADF04297 standard; protein; 555 AA.  
DE Bacterial polypeptide #410.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.5%; Score 79; DB 7; Length 555;  
Best Local Similarity 21.4%; Pred. No. 12;  
RESULT 1275  
ID AAY41118 standard; protein; 667 AA.  
DE Rice sucrose transport protein (clone rls6.pk0076.e2).  
PN WO9953068-A2.  
PD 21-OCT-1999.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
Query Match 6.5%; Score 79; DB 2; Length 667;  
Best Local Similarity 24.0%; Pred. No. 15;

RESULT 1276  
ID AAW88525 standard; protein; 1305 AA.  
DE Adenyl cyclase type 9 protein ammo acid sequence.  
PN WO9853856-A1.  
PD 03-DEC-1998.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 6.5%; Score 79; DB 2; Length 1305;  
Best Local Similarity 23.5%; Pred. No. 39;  
RESULT 1277  
ID AAR9251 standard; protein; 1353 AA.  
DE Murine adenylate cyclase 9.  
PN WO9625502-A1.  
PD 22-AUG-1996.  
PA (MEDI-) MEDICAL RES COUNCIL.  
Query Match 6.5%; Score 79; DB 2; Length 1353;  
Best Local Similarity 23.5%; Pred. No. 41;  
RESULT 1278  
ID ADE55614 standard; protein; 328 AA.  
DE Rat Protein CAA08796, SEQ ID NO 1433.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 6.5%; Score 78.5; DB 7; Length 323;  
Best Local Similarity 26.8%; Pred. No. 6.4;  
RESULT 1279  
ID ADE55610 standard; protein; 328 AA.  
DE Rat Protein CAA08796, SEQ ID NO 1429.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 6.5%; Score 78.5; DB 7; Length 328;  
Best Local Similarity 26.8%; Pred. No. 6.4;  
RESULT 1280  
ID ABP99400 standard; protein; 423 AA.  
DE Arabidopsis thaliana polypeptide SEQ ID NO 85.  
PN WO200266660-A2.  
PD 29-AUG-2002.  
PA (META-) METANOMICS GMBH & CO KGAA.  
Query Match 6.5%; Score 78.5; DB 5; Length 423;  
Best Local Similarity 20.7%; Pred. No. 9.1;  
RESULT 1281  
ID ABG24464 standard; protein; 2005 AA.  
DE Novel human diagnostic protein #24455.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.5%; Score 78.5; DB 4; Length 2005;  
Best Local Similarity 24.7%; Pred. No. 83;  
RESULT 1282  
ID ABM72364 standard; protein; 309 AA.  
DE Staphylococcus aureus protein #1604.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 6.4%; Score 78; DB 6; Length 309;  
Best Local Similarity 20.8%; Pred. No. 6.7;  
RESULT 1283  
ID ABU39954 standard; protein; 1059 AA.  
DE Protein encoded by prokaryotic essential gene #25481.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.4%; Score 78; DB 6; Length 1059;  
Best Local Similarity 23.6%; Pred. No. 38;  
RESULT 1284  
ID AAV33615 standard; protein; 1062 AA.  
DE Pseudomonas aeruginosa cellular proliferation protein #59.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.4%; Score 78; DB 4; Length 1062;

Best Local Similarity 24.5%; Pred. No. 38;  
RESULT 1285  
ID ABU15603 standard; protein; 1062 AA.  
DE Protein encoded by Prokaryotic essential gene #1130.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.4%; Score 78; DB 6; Length 1062;  
Best Local Similarity 24.5%; Pred. No. 38;  
RESULT 1286  
ID ABO82891 standard; protein; 1065 AA.  
DE Pseudomonas aeruginosa polypeptide #15066.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.4%; Score 78; DB 7; Length 1065;  
Best Local Similarity 24.5%; Pred. No. 39;  
RESULT 1287  
ID ABO77741 standard; protein; 222 AA.  
DE Pseudomonas aeruginosa polypeptide #9916.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.4%; Score 77.5; DB 7; Length 222;  
Best Local Similarity 23.6%; Pred. No. 4.8;  
RESULT 1288  
ID ADM35793 standard; protein; 315 AA.  
DE Human novel G protein-coupled receptor, GPCR1C.  
PN US2003211485-A1.  
PD 13-NOV-2003.  
PA (GERL/) GERLACH V L.  
PA (MACD/) MACDOUGALL J R.  
PA (STON/) STONE D J.  
PA (SMIT/) SMITHSON G.  
PA (PADI/) PADIGARU M.  
PA (BURG/) BURGESS C.  
PA (VERN/) VERNET C.  
PA (FERN/) FERNANDES E.  
PA (SHIM/) SHIMKETS R A.  
PA (TCH/) TCHERNEV V T.  
PA (MISH/) MISHRA V.  
PA (CASM/) CASMAN S.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B.  
Query Match 6.4%; Score 77.5; DB 7; Length 315;  
Best Local Similarity 21.1%; Pred. No. 7.8;  
RESULT 1289  
ID AAY19919 standard; protein; 416 AA.  
DE B. burgdorferi antigenic protein, t291.aa.  
PN WO9859071-A1.  
PD 30-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (MEDI-) MEDIMMUNE INC.  
Query Match 6.4%; Score 77.5; DB 2; Length 416;  
Best Local Similarity 24.3%; Pred. No. 12;  
RESULT 1290  
ID ABU25897 standard; protein; 434 AA.  
DE Protein encoded by Prokaryotic essential gene #11424.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.4%; Score 77.5; DB 6; Length 434;  
Best Local Similarity 20.8%; Pred. No. 12;  
RESULT 1291  
ID ADC77581 standard; protein; 453 AA.  
DE Mouse TMS2 amino acid sequence.  
PN WO2003066829-A2.  
PD 14-AUG-2003.  
PA (DISC-) DISCOVERY GENOMICS INC.  
Query Match 6.4%; Score 77.5; DB 7; Length 453;  
Best Local Similarity 23.5%; Pred. No. 13;  
RESULT 1292  
ID ABR62787 standard; protein; 459 AA.

DE MRSA hexose phosphate transporter SA214.  
PN WO2003062466-A2.  
PD 31-JUL-2003.  
PA (UYBR-) UNIV BRISTOL.  
Query Match 6.4%; Score 77.5; DB 7; Length 459;  
Best Local Similarity 24.2%; Pred. No. 13;  
RESULT 1293  
ID ABJ18956 standard; protein; 465 AA.  
DE Pathogen specific antigen related staphylococcal protein SEQ ID No 102.  
PN WO200259148-A2.  
PD 01-AUG-2002.  
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.  
Query Match 6.4%; Score 77.5; DB 6; Length 465;  
Best Local Similarity 24.2%; Pred. No. 14;  
RESULT 1294  
ID ABM72036 standard; protein; 465 AA.  
DE Staphylococcus aureus protein #1276.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 6.4%; Score 77.5; DB 6; Length 465;  
Best Local Similarity 24.2%; Pred. No. 14;  
RESULT 1295  
ID AAY19918 standard; protein; 500 AA.  
DE B. burgdorferi antigenic protein, f291.aa.  
PN WO9859071-A1.  
PD 30-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (MEDI-) MEDIMMUNE INC.  
Query Match 6.4%; Score 77.5; DB 2; Length 500;  
Best Local Similarity 24.3%; Pred. No. 15;  
RESULT 1296  
ID AAU50487 standard; protein; 349 AA.  
DE Propionibacterium acnes immunogenic protein #11383.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 6.3%; Score 77; DB 4; Length 349;  
Best Local Similarity 27.4%; Pred. No. 10;  
RESULT 1297  
ID ABM47006 standard; protein; 349 AA.  
DE Propionibacterium acnes transporter-related polypeptide #11682.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 6.3%; Score 77; DB 6; Length 349;  
Best Local Similarity 27.4%; Pred. No. 10;  
RESULT 1298  
ID AAU35552 standard; protein; 1032 AA.  
DE Haemophilus influenzae cellular proliferation protein #193.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.3%; Score 77; DB 4; Length 1032;  
Best Local Similarity 22.6%; Pred. No. 48;  
RESULT 1299  
ID ABU30420 standard; protein; 1032 AA.  
DE Protein encoded by Prokaryotic essential gene #15947.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.3%; Score 77; DB 6; Length 1032;  
Best Local Similarity 22.6%; Pred. No. 48;  
RESULT 1300  
ID AAG30768 standard; protein; 1200 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36843.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.3%; Score 77; DB 3; Length 1200;  
Best Local Similarity 28.4%; Pred. No. 60;  
RESULT 1301  
ID AAG30767 standard; protein; 1207 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36842.

PN EPI033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 6.3%; Score 77; DB 3; Length 1207;  
 RESULT 1302  
 ID AAG30766 standard; protein; 1215 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 36841.  
 PN EPI033405-A2.  
 PD 06-SEP-2000.  
 Query Match  
 Best Local Similarity 6.3%; Score 77; DB 3; Length 1215;  
 RESULT 1303  
 ID ABB71131 standard; protein; 426 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 40185.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match  
 Best Local Similarity 6.3%; Score 76.5; DB 4; Length 426;  
 RESULT 1304  
 ID ABP73987 standard; protein; 468 AA.  
 DE Candida albicans essential protein SEQ ID NO 7824.  
 PN WO200253728-A2.  
 PD 11-JUL-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match  
 Best Local Similarity 6.3%; Score 76.5; DB 5; Length 468;  
 RESULT 1305  
 ID AAY41125 standard; protein; 563 AA.  
 DE Wheat sucrose transport protein (clone wlmk1.pk0002.e11).  
 PN WO9953068-A2.  
 PD 21-OCT-1999.  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 Query Match  
 Best Local Similarity 6.3%; Score 76.5; DB 2; Length 563;  
 RESULT 1306  
 ID ABO66088 standard; protein; 614 AA.  
 DE Klebsiella pneumoniae polypeptide seqid 12605.  
 PN US610836-B1.  
 PD 26-AUG-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 6.3%; Score 76.5; DB 7; Length 614;  
 RESULT 1307  
 ID ABP71102 standard; protein; 1378 AA.  
 DE Murine homologue of attractin/mahogany (HAM) polypeptide.  
 PN WO200297120-A1.  
 PD 05-DEC-2002.  
 PA (IMMV ) IMMUNEX CORP.  
 Query Match  
 Best Local Similarity 6.3%; Score 76.5; DB 6; Length 1378;  
 RESULT 1308  
 ID ABB98398 standard; protein; 19938 AA.  
 DE Streptomyces viridochromogenes Av1 gene cluster polypeptide frame 1.  
 PN WO200268436-A1.  
 PD 06-SEP-2002.  
 PA (COMB-) COMBINATURE BIOPHARM AG.  
 Query Match  
 Best Local Similarity 6.3%; Score 76.5; DB 6; Length 19938;  
 RESULT 1309  
 ID AAM56388 standard; protein; 315 AA.  
 DE Fragment of the human GYT-2 transporter encoded by clone phG2-9b.  
 PN WO9807854-A1.  
 PD 26-FEB-1998.  
 PA (ALLX ) ALLELIX NEUROSCIENCE INC.  
 Query Match  
 Best Local Similarity 6.3%; Score 76; DB 2; Length 315;  
 RESULT 1310  
 ID AAG81675 standard; protein; 337 AA.  
 DE S. epidermidis open reading frame protein sequence SEQ ID NO:444.  
 PN WO200134809-A2.  
 PD 17-MAY-2001.  
 PA (GLAX ) GLAXO GROUP LTD.

Query Match  
 Best Local Similarity 6.3%; Score 76; DB 4; Length 337;  
 RESULT 1311  
 ID ABB48085 standard; protein; 431 AA.  
 DE Listeria monocytogenes protein #789.  
 PN WO200177335-A2.  
 PD 18-OCT-2001.  
 PA (INSP ) INST PASTEUR.  
 Query Match  
 Best Local Similarity 6.3%; Score 76; DB 5; Length 431;  
 RESULT 1312  
 ID ABM73417 standard; protein; 447 AA.  
 DE Staphylococcus aureus protein #2657.  
 PN WO200294868-A2.  
 PD 28-NOV-2002.  
 PA (CHIR-) CHIRON SPA.  
 Query Match  
 Best Local Similarity 6.3%; Score 76; DB 6; Length 447;  
 RESULT 1313  
 ID ABG10541 standard; protein; 480 AA.  
 DE Novel human diagnostic protein #10532.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match  
 Best Local Similarity 6.3%; Score 76; DB 4; Length 480;  
 RESULT 1314  
 ID ADF04316 standard; protein; 500 AA.  
 DE Bacterial polypeptide #429.  
 PN US6605709-B1.  
 PD 12-AUG-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 6.3%; Score 76; DB 7; Length 500;  
 RESULT 1315  
 ID AAB61263 standard; protein; 631 AA.  
 DE Human monocyte inhibitory receptor precursor.  
 PN WO200100810-A1.  
 PD 04-JAN-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match  
 Best Local Similarity 6.3%; Score 76; DB 4; Length 631;  
 RESULT 1316  
 ID ABT19062 standard; protein; 643 AA.  
 DE Pathogen specific antigen related staphylococcal protein seq ID NO 339.  
 PN WO200259148-A2.  
 PD 01-AUG-2002.  
 PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.  
 Query Match  
 Best Local Similarity 6.3%; Score 76; DB 6; Length 643;  
 RESULT 1317  
 ID ABB71337 standard; protein; 1079 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 40803.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match  
 Best Local Similarity 6.3%; Score 76; DB 4; Length 1079;  
 RESULT 1318  
 ID ADB10794 standard; protein; 93 AA.  
 DE Alloiococcus ostitis antigenic protein SEQ ID NO:4266.  
 PN WO2003048304-A2.  
 PD 12-JUN-2003.  
 PA (AMHP ) WYETH HOLDINGS CORP.  
 Query Match  
 Best Local Similarity 6.2%; Score 75.5; DB 6; Length 93;  
 RESULT 1319  
 ID ADB10762 standard; protein; 93 AA.  
 DE Alloiococcus ostitis antigenic protein SEQ ID NO:4298.  
 PN WO2003048304-A2.  
 PD 12-JUN-2003.  
 PA (AMHP ) WYETH HOLDINGS CORP.  
 Query Match  
 Best Local Similarity 6.2%; Score 75.5; DB 6; Length 93;



Best Local Similarity 31.4%; Pred. No. 2.4;  
RESULT 1320  
ID ADB1392 standard; protein; 93 AA.  
DE Alloiococcus otitis antigenic protein SEQ ID NO:5668.  
PN WO2003048304-A2.  
PD 12-JUN-2003.  
PA (AMHP ) WYETH HOLDINGS CORP.  
Query Match 6.2%; Score 75.5; DB 6; Length 93;  
Best Local Similarity 31.4%; Pred. No. 2.4;  
RESULT 1321  
ID ABP63103 standard; protein; 397 AA.  
DE FLO11 gene expression regulator At18.  
PN WO200257456-A2.  
PD 25-JUL-2002.  
PA (MICR-) MICROBIA.  
Query Match 6.2%; Score 75.5; DB 5; Length 397;  
Best Local Similarity 26.3%; Pred. No. 19;  
RESULT 1322  
ID ABP35575 standard; protein; 397 AA.  
DE Fungal ZBC protein sequence #1.  
PN WO200224865-A2.  
PD 28-MAR-2002.  
PA (MICR-) MICROBIA INC.  
Query Match 6.2%; Score 75.5; DB 5; Length 397;  
Best Local Similarity 26.3%; Pred. No. 19;  
RESULT 1323  
ID ABU49908 standard; protein; 409 AA.  
DE Protein encoded by Prokaryotic essential gene #35435.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.2%; Score 75.5; DB 6; Length 409;  
Best Local Similarity 23.2%; Pred. No. 19;  
RESULT 1324  
ID ADN73661 standard; protein; 476 AA.  
DE Thale cress protein repressed in E2Fa/Dpa expressing plants SegID 1556.  
PN WO2004035798-A2.  
PD 29-APR-2004.  
PA (CROP-) CROPPDESIGN NV.  
Query Match 6.2%; Score 75.5; DB 8; Length 476;  
Best Local Similarity 21.5%; Pred. No. 24;  
RESULT 1325  
ID ADA36649 standard; protein; 277 AA.  
DE Acinetobacter baumannii protein #3810.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.2%; Score 75; DB 6; Length 277;  
Best Local Similarity 39.2%; Pred. No. 13;  
RESULT 1326  
ID ABB98338 standard; protein; 292 AA.  
DE Human anti-tenascin C monoclonal antibody SEQ ID NO 2.  
PN JP2002234900-A.  
PD 23-AUG-2002.  
PA (MIED-) MIE DAIGAKUCHO.  
Query Match 6.2%; Score 75; DB 6; Length 292;  
Best Local Similarity 34.7%; Pred. No. 14;  
RESULT 1327  
ID ADP04284 standard; protein; 292 AA.  
DE Human tenascin C fibronectin III-like domain BCD domain polypeptide.  
PN JP2004138489-A.  
PD 13-MAY-2004.  
PA (MENE-) MENEKI SEIBUTSU KENKYUSHO KK.  
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIYUTSU SH.  
Query Match 6.2%; Score 75; DB 8; Length 292;  
Best Local Similarity 34.7%; Pred. No. 14;  
RESULT 1328  
ID ABU29147 standard; protein; 527 AA.  
DE Protein encoded by Prokaryotic essential gene #14674.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.2%; Score 75; DB 6; Length 527;

Best Local Similarity 21.2%; Pred. No. 32;  
RESULT 1329  
ID ADN05803 standard; protein; 2000 AA.  
DE Antipsoriatic protein sequence #1065.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 6.2%; Score 75; DB 8; Length 2000;  
Best Local Similarity 34.7%; Pred. No. 2.1e+02;  
RESULT 1330  
ID ABO01379 standard; protein; 2108 AA.  
DE Human protein NOV35b.  
PN WO2003023008-A2.  
PD 20-MAR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.2%; Score 75; DB 6; Length 2108;  
Best Local Similarity 34.7%; Pred. No. 2.3e+02;  
RESULT 1331  
ID ADN96130 standard; protein; 2108 AA.  
DE Human NOVX polypeptide #92.  
PN US2004067490-A1.  
PD 08-APR-2004.  
PA (ZHON/) ZHONG M.  
PA (LIL/) LI L.  
PA (GORM/) GORMAN L.  
PA (SPYT/) SPYTEK K A.  
PA (KEKU/) KEKUDA R.  
PA (TAUP/) TAUPIER R J.  
PA (ANDE/) ANDERSON D W.  
PA (VERN/) VERNET C A M.  
PA (CATT/) CATTERTON E.  
PA (MILL/) MILLER C E.  
PA (SHEN/) SHENOY S G.  
PA (PAT/) PATURAJAN M.  
PA (PENA/) PENNA C E A.  
PA (TCHE/) TCHEURNEV V T.  
PA (PADI/) PADIGARU M.  
PA (GUSE/) GUSEV V Y.  
PA (MALY/) MALYANKAR U M.  
PA (BURG/) BURGESS C E.  
PA (GERL/) GERLACH V.  
PA (CASM/) CASMAN S J.  
PA (RIEG/) RIEGER D K.  
PA (GROS/) GROSSE W M.  
PA (SMIT/) SMITHSON G.  
PA (PEYM/) PEYMAN J A.  
PA (STAR/) STARLING G.  
PA (ROTH/) ROTHENBERG M E.  
PA (LARO/) LAROCHELLE W J.  
PA (SHIM/) SHIMKETS R A.  
PA (CRAB/) CRABTREE J.  
PA (RAST/) RASTELLI L.  
PA (VOSS/) VOSS E Z.  
PA (BOLD/) BOLDOG F L.  
PA (EDIN/) EDINGER S R.  
PA (MILL/) MILLER I.  
PA (MACD/) MACDOUGALL J R.  
PA (ELIE/) ELLERMAN K.  
PA (CHAP/) CHAPOVAL A.  
Query Match 6.2%; Score 75; DB 8; Length 2108;  
Best Local Similarity 34.7%; Pred. No. 2.3e+02;  
RESULT 1332  
ID AAO30847 standard; protein; 2110 AA.  
DE Human cell adhesion and extracellular matrix protein (CADECM)-37.  
PN WO2003047526-A2.  
PD 12-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 6.2%; Score 75; DB 7; Length 2110;  
Best Local Similarity 34.7%; Pred. No. 2.3e+02;  
RESULT 1333  
ID ADM80773 standard; protein; 2110 AA.  
DE Human CADECM-2 protein SEQ ID NO:2.  
PN WO2004015396-A2.

PD 19-FEB-2004.  
PA (INCY-) INCYTE CORP.  
Query Match  
Best Local Similarity 34.7%; Score 75; DB 8; Length 2110;  
RESULT 1334  
ID ABG70361 standard; protein; 2167 AA.  
DE Novel human thrombopoietin variant protein, NV-20.  
PN US2002068342-A1.  
PD 06-JUN-2002.  
PA (KHOS/) KHOSRAVI R.  
PA (BERN/) BERNSTEIN J.  
Query Match  
Best Local Similarity 34.7%; Score 75; DB 5; Length 2167;  
RESULT 1335  
ID AAR94562 standard; protein; 2199 AA.  
DE Human cytotactin.  
PN WO9608513-A1.  
PD 21-MAR-1996.  
PA (SCRI ) SCRIPPS RES INST.  
Query Match  
Best Local Similarity 34.7%; Score 75; DB 2; Length 2199;  
RESULT 1336  
ID ABO01378 standard; protein; 2199 AA.  
DE Human protein NOV35a.  
PN WO2003023008-A2.  
PD 20-MAR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 34.7%; Score 75; DB 6; Length 2199;  
RESULT 1337  
ID ADN96128 standard; protein; 2199 AA.  
DE Human NOVX polypeptide #91.  
PN US2004067490-A1.  
PD 08-APR-2004.  
PA (ZHON/) ZHONG M.  
PA (LILL/) LI L.  
PA (GORM/) GORMAN L.  
PA (SPYT/) SPYTEK K A.  
PA (KEKU/) KEKUDA R.  
PA (TAUP/) TAUPIER R J.  
PA (ANDE/) ANDERSON D W.  
PA (VERN/) VERNET C A M.  
PA (CATT/) CATTERTON E.  
PA (MILL/) MILLER C E.  
PA (SHEN/) SHENOY S G.  
PA (PATT/) PATTURAJAN M.  
PA (PENA/) PENNA C E A.  
PA (TCHE/) TCHERNEV V T.  
PA (PADI/) PADIGARU M.  
PA (GUSE/) GUSEV V Y.  
PA (MALY/) MALYANKAR U M.  
PA (BURG/) BURGESS C E.  
PA (GERL/) GERLACH V.  
PA (CASM/) CASMAN S J.  
PA (RIEG/) RIEGER D K.  
PA (GROS/) GROSSE W M.  
PA (SMIT/) SMITHSON G.  
PA (PEYM/) PEYMAN J A.  
PA (STAR/) STARLING G.  
PA (ROTH/) ROTHENBERG M E.  
PA (LARO/) LAROCHELLE W J.  
PA (SHIM/) SHIMKETS R A.  
PA (CRAB/) CRABTREE J.  
PA (RAST/) RASTELLI L.  
PA (VOSS/) VOSS E Z.  
PA (BOLD/) BOLDOG F L.  
PA (EDIN/) EDINGER S R.  
PA (MILL/) MILLET I.  
PA (MACD/) MACDOUGALL J R.  
PA (ELLE/) ELLERMAN K.  
PA (CHAP/) CHAPOVAL A.  
Query Match  
Best Local Similarity 34.7%; Score 75; DB 8; Length 2199;  
34.7%; Pred. No. 2.4e+02;

RESULT 1338  
ID AAB36935 standard; protein; 2201 AA.  
DE Human tenascin-C.  
PN WO200066628-A1.  
PD 09-NOV-2000.  
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
Query Match  
Best Local Similarity 34.7%; Score 75; DB 4; Length 2201;  
RESULT 1339  
ID ABP97745 standard; protein; 2201 AA.  
DE Amino acid sequence of human HXB polypeptide.  
PN WO2003010205-A1.  
PD 06-FEB-2003.  
PA (UYDU-) UNIV DUKE MEDICAL CENT.  
Query Match  
Best Local Similarity 34.7%; Score 75; DB 6; Length 2201;  
RESULT 1340  
ID ABM78955 standard; protein; 2201 AA.  
DE Breast cancer specific marker under-expressed in breast cancer.  
PN WO2003073911-A2.  
PD 12-SEP-2003.  
PA (GEOU ) UNIV GEORGETOWN.  
Query Match  
Best Local Similarity 34.7%; Score 75; DB 7; Length 2201;  
RESULT 1341  
ID ADD69400 standard; protein; 2201 AA.  
DE Human tenascin protein - SEQ ID NO 136.  
PN WO2003048185-A2.  
PD 12-JUN-2003.  
PA (GENV-) GENVEC INC.  
Query Match  
Best Local Similarity 34.7%; Score 75; DB 7; Length 2201;  
RESULT 1342  
ID ADD47935 standard; protein; 2201 AA.  
DE Human Protein XP\_005348, SEQ ID NO 13631.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match  
Best Local Similarity 34.7%; Score 75; DB 7; Length 2201;  
RESULT 1343  
ID ADE62224 standard; protein; 2201 AA.  
DE Human Protein P24821, SEQ ID NO 8153.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match  
Best Local Similarity 34.7%; Score 75; DB 7; Length 2201;  
RESULT 1344  
ID ADO17766 standard; protein; 2201 AA.  
DE Differentially expressed protein Lul, SEQ ID 1.  
PN WO2004015390-A2.  
PD 19-FEB-2004.  
PA (APPL-) APPLERA CORP.  
Query Match  
Best Local Similarity 34.7%; Score 75; DB 8; Length 2201;  
RESULT 1345  
ID ADQ19756 standard; protein; 2201 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2575.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 34.7%; Score 75; DB 8; Length 2201;  
RESULT 1346  
ID AAM41065 standard; protein; 210 AA.  
DE Human polypeptide SEQ ID NO 5996.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
6.1%; Score 74.5; DB 4; Length 210;  
34.7%; Pred. No. 2.4e+02;

Best Local Similarity 22.8%; Pred. No. 9.9;  
RESULT 1347  
ID AAM41066 standard; protein; 210 AA.  
DE Human polypeptide SEQ ID NO 5997.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.1%; Score 74.5; DB 4; Length 210;  
Best Local Similarity 22.8%; Pred. No. 9.9;  
RESULT 1348  
ID AAM41067 standard; protein; 210 AA.  
DE Human polypeptide SEQ ID NO 5998.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.1%; Score 74.5; DB 4; Length 210;  
Best Local Similarity 22.8%; Pred. No. 9.9;  
RESULT 1349  
ID AAB46359 standard; protein; 255 AA.  
DE H. pylori HPC104 protein.  
PN WO200073502-A2.  
PD 07-DEC-2000.  
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
PA (CREA-) CREATOGEN GMBH.  
Query Match 6.1%; Score 74.5; DB 4; Length 255;  
Best Local Similarity 18.6%; Pred. No. 13;  
RESULT 1350  
ID ABP58049 standard; protein; 289 AA.  
DE Saccharomyces cerevisiae aquaporin.  
PN WO200290557-A2.  
PD 14-NOV-2002.  
PA (VLAA-) VLAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
Query Match 6.1%; Score 74.5; DB 6; Length 289;  
Best Local Similarity 26.8%; Pred. No. 16;  
RESULT 1351  
ID AAB78974 standard; protein; 364 AA.  
DE C. glutamicum SRT protein sequence SEQ ID NO:208.  
PN WO200100804-A2.  
PD 04-JAN-2001.  
PA (BADI ) BASF AG.  
Query Match 6.1%; Score 74.5; DB 4; Length 364;  
Best Local Similarity 20.3%; Pred. No. 21;  
RESULT 1352  
ID AAG92975 standard; protein; 378 AA.  
DE C glutamicum protein fragment SEQ ID NO: 6729.  
PN EPI108790-A2.  
PD 20-JUN-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match 6.1%; Score 74.5; DB 4; Length 378;  
Best Local Similarity 20.3%; Pred. No. 23;  
RESULT 1353  
ID AAB78973 standard; protein; 412 AA.  
DE C. glutamicum SRT protein sequence SEQ ID NO:206.  
PN WO200100804-A2.  
PD 04-JAN-2001.  
PA (BADI ) BASF AG.  
Query Match 6.1%; Score 74.5; DB 4; Length 412;  
Best Local Similarity 20.3%; Pred. No. 26;  
RESULT 1354  
ID ABU49116 standard; protein; 468 AA.  
DE Protein encoded by Prokaryotic essential gene #34643.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.1%; Score 74.5; DB 6; Length 468;  
Best Local Similarity 25.7%; Pred. No. 31;  
RESULT 1355  
ID ABB60065 standard; protein; 473 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 6987.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 6.1%; Score 74.5; DB 4; Length 473;

Best Local Similarity 16.5%; Pred. No. 31;  
RESULT 1356  
ID AAU18057 standard; protein; 524 AA.  
DE Human immunoglobulin polypeptide SEQ ID NO 202.  
PN WO200155315-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.1%; Score 74.5; DB 4; Length 524;  
Best Local Similarity 22.2%; Pred. No. 36;  
RESULT 1357  
ID ABB10423 standard; protein; 524 AA.  
DE Human cDNA SEQ ID NO: 731.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.1%; Score 74.5; DB 4; Length 524;  
Best Local Similarity 22.2%; Pred. No. 36;  
RESULT 1358  
ID ABP67010 standard; protein; 524 AA.  
DE Human polypeptide SEQ ID NO 731.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 6.1%; Score 74.5; DB 5; Length 524;  
Best Local Similarity 22.2%; Pred. No. 36;  
RESULT 1359  
ID ADB31681 standard; protein; 524 AA.  
DE Human novel protein SEQ ID NO 202.  
PN US2003077606-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.1%; Score 74.5; DB 7; Length 524;  
Best Local Similarity 22.2%; Pred. No. 36;  
RESULT 1360  
ID ABU20338 standard; protein; 541 AA.  
DE Protein encoded by Prokaryotic essential gene #5865.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.1%; Score 74.5; DB 6; Length 541;  
Best Local Similarity 20.3%; Pred. No. 38;  
RESULT 1361  
ID ABB90801 standard; protein; 618 AA.  
DE Herbicidially active polypeptide SEQ ID NO 12.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB ) BAYER AG.  
Query Match 6.1%; Score 74.5; DB 5; Length 618;  
Best Local Similarity 27.7%; Pred. No. 46;  
RESULT 1362  
ID ADN74317 standard; protein; 618 AA.  
DE Thale cress protein repressed in E2Fa/Dpa expressing plants SegID 2212.  
PN WO2004035798-A2.  
PD 29-APR-2004.  
PA (CROP-) CROPPDESIGN NV.  
Query Match 6.1%; Score 74.5; DB 8; Length 618;  
Best Local Similarity 27.7%; Pred. No. 46;  
RESULT 1363  
ID ABB10186 standard; protein; 654 AA.  
DE Human cDNA SEQ ID NO: 494.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.1%; Score 74.5; DB 4; Length 654;  
Best Local Similarity 22.2%; Pred. No. 49;  
RESULT 1364  
ID ABP66773 standard; protein; 654 AA.  
DE Human polypeptide SEQ ID NO 494.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match  
Best Local Similarity 22.2%; Pred. No. 49; Length 654;  
RESULT 1365  
ID ADP04132 standard; protein; 705 AA.  
DE Human colon specific protein SEQ ID NO:113.  
PN WO2004050858-A2.  
PD 17-JUN-2004.  
PA (DIAD-) DIADEXUS INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 55; Length 705;  
RESULT 1366  
ID AAG38915 standard; protein; 1030 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48077.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 27.7%; Pred. No. 94; Length 1030;  
RESULT 1367  
ID AAG38914 standard; protein; 1133 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48076.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 27.7%; Pred. No. 1.1e+02; Length 1133;  
RESULT 1368  
ID AAG38913 standard; protein; 1193 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48075.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 27.7%; Pred. No. 1.2e+02; Length 1193;  
RESULT 1369  
ID ABU79090 standard; protein; 1709 AA.  
DE Human sialic acid binding Ig-superfamily lectin, siglec-1.  
PN US2002177551-A1.  
PD 28-NOV-2002.  
PA (TERM/) TERMAN D S.  
Query Match  
Best Local Similarity 22.2%; Pred. No. 1.9e+02; Length 1709;  
RESULT 1370  
ID ADF4331 standard; protein; 1709 AA.  
DE Superantigen associated protein seq id 51.  
PN US2003157113-A1.  
PD 21-AUG-2003.  
PA (TERM/) TERMAN D S.  
Query Match  
Best Local Similarity 22.2%; Pred. No. 1.9e+02; Length 1709;  
RESULT 1371  
ID ADJ69756 standard; protein; 1709 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1562.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match  
Best Local Similarity 22.2%; Pred. No. 1.9e+02; Length 1709;  
RESULT 1372  
ID ADH71514 standard; protein; 1709 AA.  
DE Human protein of the invention NOV14g SEQ ID NO:410.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 22.2%; Pred. No. 1.9e+02; Length 1709;  
RESULT 1373  
ID ABG01737 standard; protein; 161 AA.  
DE Novel human diagnostic protein #1728.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
6.1%; Score 74; DB 5; Length 654;  
Score 74; DB 4; Length 161;

Best Local Similarity 30.0%; Pred. No. 7.7;  
RESULT 1374  
ID AAB92492 standard; protein; 448 AA.  
DE Human protein sequence SEQ ID NO:10589.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match  
Best Local Similarity 23.5%; Pred. No. 33; Length 448;  
RESULT 1375  
ID ABB97449 standard; protein; 448 AA.  
DE Novel human protein SEQ ID NO: 717.  
PN WO200222660-A2.  
PD 21-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 23.5%; Pred. No. 33; Length 448;  
RESULT 1376  
ID ABB82639 standard; protein; 448 AA.  
DE Human hypothetical protein FLJ10060.  
PN WO200286060-A2.  
PD 31-OCT-2002.  
PA (IMME-) IMMERGE BIOTHERAPEUTICS INC.  
Query Match  
Best Local Similarity 23.5%; Pred. No. 33; Length 448;  
RESULT 1377  
ID ABB92535 standard; protein; 555 AA.  
DE Herbicidally active polypeptide SEQ ID NO 1746.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB ) BAYER AG.  
Query Match  
Best Local Similarity 26.4%; Pred. No. 45; Length 555;  
RESULT 1378  
ID ADG42638 standard; protein; 857 AA.  
DE Rat prominin.  
PN US2003204052-A1.  
PD 30-OCT-2003.  
PA (HERR/) HERRMANN J L.  
PA (RAST/) RASTELLI L.  
PA (SHIM/) SHIMKETS R A.  
Query Match  
Best Local Similarity 23.0%; Pred. No. 83; Length 857;  
RESULT 1379  
ID AAB40566 standard; protein; 261 AA.  
DE Human ORFX ORF330 polypeptide sequence SEQ ID NO:660.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1380  
ID AAY70675 standard; protein; 261 AA.  
DE Human stomach protein zsig28.  
PN WO200015659-A2.  
PD 23-MAR-2000.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1381  
ID AAY92235 standard; protein; 261 AA.  
DE Claudin homologue from clone 3224646 cDNA.  
PN WO200020447-A2.  
PD 13-APR-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1382  
ID AAY99432 standard; protein; 261 AA.  
DE Human PRO1572 (UNQ778) amino acid sequence SEQ ID NO:326.  
PN WO200012708-A2.  
PD 09-MAR-2000.  
PA (GETH ) GENENTECH INC.  
Query Match  
6.0%; Score 73.5; DB 3; Length 261;  
Score 73.5; DB 3; Length 261;

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Query Match
Best Local Similarity 23.8%; Score 73.5; DB 3; Length 261;
RESULT 1383
ID AAB6181 standard; protein; 261 AA.
DE Protein of the invention #93.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 4; Length 261;
RESULT 1384
ID AAU29201 standard; protein; 261 AA.
DE Human PRO polypeptide sequence #178.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 4; Length 261;
RESULT 1385
ID AAB87584 standard; protein; 261 AA.
DE Human PRO1572.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 4; Length 261;
RESULT 1386
ID ABG60912 standard; protein; 261 AA.
DE Protein encoded by lung specific gene #2.
PN WO200218576-A2.
PD 07-MAR-2002.
PA (DIAD-) DIADEXUS INC.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 5; Length 261;
RESULT 1387
ID ABG95909 standard; protein; 261 AA.
DE Human secreted/transmembrane protein PRO1572.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 5; Length 261;
RESULT 1388
ID ABU58577 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1389
ID ABU88125 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1390
ID ABU84440 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1391
ID ABR66314 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1392
ID ABR65704 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN 06-MAR-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1393
ID ABU9644 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1394
ID ABU82883 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1395
ID ABU90004 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1396
ID ABR68253 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1397
ID ABU96306 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1398
ID ABU92737 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1399
ID ABC08814 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1400
ID ABC02866 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1401
ID ABR75020 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1402
ID ABR94782 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
PD 06-MAR-2003.
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Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1403  
ID ABU85755 standard; protein; 261 AA.  
DE Human PRO polypeptide #178.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1404  
ID ABU98915 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1405  
ID ABU98130 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1406  
ID ABU91836 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1407  
ID ABU89529 standard; protein; 261 AA.  
DE Human PRO polypeptide #178.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1408  
ID ABU86370 standard; protein; 261 AA.  
DE Human secreted/transmembrane protein (PRO) #178.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1409  
ID ABU67583 standard; protein; 261 AA.  
DE Human secreted/transmembrane protein (PRO) #178.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1410  
ID ABU80611 standard; protein; 261 AA.  
DE Human PRO protein #178.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1411  
ID ABU90934 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1412  
ID ABO33993 standard; protein; 261 AA.  
DE Human secreted/transmembrane protein PRO1572.  
PN US2003009013-A1.

PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1413  
ID ABR99529 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1414  
ID ABR98919 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1415  
ID ABO16442 standard; protein; 261 AA.  
DE Human secreted/transmembrane protein (PRO) #178.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1416  
ID ABR92342 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1417  
ID ABO18983 standard; protein; 261 AA.  
DE Human secreted/transmembrane protein (PRO) #178.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1418  
ID ABR78404 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1419  
ID ABU72010 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1420  
ID ABU85140 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1421  
ID ABO00279 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1422  
ID ABO11611 standard; protein; 261 AA.  
DE Human secreted/transmembrane protein (PRO) #178.  
PN US2003036124-A1.

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PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1423
ID ABO02256 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1424
ID ABU88830 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1425
ID ABU83525 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1426
ID ABO06326 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1427
ID ABR59362 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1428
ID ABO09424 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1429
ID ABO19288 standard; protein; 261 AA.
DE Novel human secreted and transmembrane protein PRO1572.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1430
ID ABO11306 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1431
ID ABR66924 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1432
ID ABO16137 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
PD 06-MAR-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1433
ID ABO13843 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1434
ID ABU71564 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1435
ID ABU65746 standard; protein; 261 AA.
DE Human secreted/transmembrane protein, SEQ ID 356.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1436
ID ABO07594 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1437
ID ABO03781 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1438
ID ABR67229 standard; protein; 261 AA.
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1439
ID ABO15832 standard; protein; 261 AA.
DE Human secreted/transmembrane protein (PRO) #178.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1440
ID ABU56113 standard; protein; 261 AA.
DE Human secreted/transmembrane protein, PRO1572.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1441
ID ABU72345 standard; protein; 261 AA.
DE Human PRO polypeptide #59.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
RESULT 1442
ID ABU65441 standard; protein; 261 AA.
DE Human PRO polypeptide #178.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 23.8%; Score 73.5; DB 6; Length 261;
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Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1443  
ID ABU95386 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1444  
ID ABU71289 standard; protein; 261 AA.  
DE Human PRO1572 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1445  
ID ABO07899 standard; protein; 261 AA.  
DE Human PRO polypeptide #178.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1446  
ID ABR70140 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1447  
ID ABR69473 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1448  
ID ABO01614 standard; protein; 261 AA.  
DE Human PRO polypeptide #178.  
PN US200308353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1449  
ID ABU81416 standard; protein; 261 AA.  
DE Human PRO polypeptide #178.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1450  
ID ABR60213 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1451  
ID ABU91018 standard; protein; 261 AA.  
DE Human PRO polypeptide #59.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1452  
ID ABR67948 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;

Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1453  
ID ABR65336 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1454  
ID ABR68558 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1455  
ID ABR71970 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1456  
ID ABU85450 standard; protein; 261 AA.  
DE Human PRO polypeptide #178.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1457  
ID ABU89140 standard; protein; 261 AA.  
DE Human secreted/transmembrane protein (PRO) #178.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1458  
ID ABU83220 standard; protein; 261 AA.  
DE Human secreted/transmembrane protein (PRO) #178.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1459  
ID ABU95076 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1460  
ID ABU90624 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1461  
ID ABU84135 standard; protein; 261 AA.  
DE Human secreted/transmembrane protein (PRO) #178.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1462  
ID ABU93786 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1463  
ID ABU93786 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1464  
ID ABU93786 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;  
RESULT 1465  
ID ABU93786 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 6.0%; Score 73.5; DB 6; Length 261;

RESULT 1463  
ID ABR65031 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1464  
ID ABO27339 standard; protein; 261 AA.  
DE Human secreted/transmembrane polypeptide PRO1572.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1465  
ID ABR68863 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1466  
ID ABO06679 standard; protein; 261 AA.  
DE Human secreted/transmembrane protein (PRO) #178.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1467  
ID ABR99224 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1468  
ID ABU57108 standard; protein; 261 AA.  
DE Human PRO polypeptide #178.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1469  
ID ABU86060 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1470  
ID ABU82347 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1471  
ID ABU87358 standard; protein; 261 AA.  
DE Human PRO polypeptide #178.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1472  
ID ABU83830 standard; protein; 261 AA.  
DE Human secreted/transmembrane protein (PRO) #178.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1473  
ID ABO08204 standard; protein; 261 AA.

DE Human PRO polypeptide #178.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1474  
ID ABU92534 standard; protein; 261 AA.  
DE Human secreted/transmembrane protein PRO1572.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1475  
ID ABU81915 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1476  
ID ABU66079 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1477  
ID ABU81204 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1478  
ID ABR59908 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1479  
ID ABU94096 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1480  
ID ABU99949 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1481  
ID ABR66619 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1482  
ID ABR91037 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 23.8%; Pred. No. 18; Length 261;  
RESULT 1483  
ID ABO53318 standard; protein; 261 AA.

DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1484  
ID ABU94464 standard; protein; 261 AA.  
DE Human PRO polypeptide #178.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1485  
ID ABU79346 standard; protein; 261 AA.  
DE Human PRO polypeptide #178.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1486  
ID ABU86675 standard; protein; 261 AA.  
DE Human secreted/transmembrane protein (PRO) #178.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1487  
ID ABU86980 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1488  
ID ABU94769 standard; protein; 261 AA.  
DE Human PRO polypeptide #178.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1489  
ID ABO04696 standard; protein; 261 AA.  
DE Human PRO polypeptide #178.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1490  
ID ABR70445 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1491  
ID ABU98610 standard; protein; 261 AA.  
DE Human PRO polypeptide #178.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1492  
ID ABR66009 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1493  
ID ABR64726 standard; protein; 261 AA.  
DE Human secreted polypeptide PRO1572, SEQ ID NO:356.

PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1494  
ID ABU79651 standard; protein; 261 AA.  
DE Human PRO polypeptide #178.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1495  
ID ABU93042 standard; protein; 261 AA.  
DE Human secreted/transmembrane protein (PRO) #178.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1496  
ID ABU96001 standard; protein; 261 AA.  
DE Human PRO polypeptide #178.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1497  
ID ABU91221 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1498  
ID ABU90314 standard; protein; 261 AA.  
DE Novel human secreted and transmembrane protein PRO1572.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1499  
ID ABO09729 standard; protein; 261 AA.  
DE Human secreted/transmembrane protein (PRO) #178.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;  
RESULT 1500  
ID ABO11001 standard; protein; 261 AA.  
DE Human secreted/transmembrane protein (PRO) #178.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 6.0%; Score 73.5; DB 6; Length 261;  
Best Local Similarity 23.8%; Pred. No. 18;